

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:38:24 ; Search time 3711.97 Seconds
(without alignments)
11219.411 Million cell updates/sec

Title: US-09-576-424-3
Perfect score: 1431
Sequence: 1 atgaacacccgtgtgtttttt.....ccctgtctccgggtaaatga 1431

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.vi.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.rod.*

36: em.htg.mam.*

37: em.htg.vrt.*

38: em.sy.*

39: em.htgo.hum.*

40: em.htgo.mus.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1431	100.0	1431	6	AR108863 Sequence
2	1315.8	91.9	1431	6	AR108867 Sequence
3	1237.2	86.5	1431	6	E10697 cDNA encodi
4	1234.8	86.3	1567	6	AR135359 Sequence
5	1227.6	85.8	1596	6	AK098516 Homo sapi
6	1221.6	85.4	1418	6	A49389 Sequence 7
7	1215.2	84.9	1594	9	AK057754 Homo sapi
8	1210.4	84.6	1418	6	AR176296 Sequence
9	1209.6	84.5	1589	9	AK057775 Homo sapi
10	1171.4	81.9	1404	6	AR135375 Sequence
11	1170	81.8	1566	9	AK097365 Homo sapi
12	1168.2	81.6	1404	6	AR135377 Sequence
13	1166.6	81.5	1404	6	AR135376 Sequence
14	1125.8	78.7	1633	9	AK097859 Homo sapi
15	1124.2	78.6	1507	6	BD000501 Process f
16	1123.6	78.5	1428	6	AR031184 Sequence
17	1123.6	78.5	1428	6	AR042589 Sequence
18	1123.6	78.5	1428	6	AR059282 Sequence
19	1123.6	78.5	1428	6	AR076260 Sequence
20	1122.8	78.5	1430	6	AX119496 Sequence
21	1117.4	78.1	1679	9	BC018747 Homo sapi
22	1117.2	78.1	1437	6	AR108865 Sequence
23	1116.2	78.0	1624	9	HSIGG1KH
24	1115.4	77.9	1630	9	BC024289 Homo sapi
25	1113.2	77.8	1673	9	HSIGG1LH
26	1113.2	77.8	3143	9	BC019046 Homo sapi
27	1112.4	77.7	1428	6	AR031186 Sequence
28	1112.4	77.7	1428	6	AR042591 Sequence
29	1112.4	77.7	1428	6	AR059284 Sequence
30	1112.4	77.7	1428	6	AR076262 Sequence
31	1112.4	77.7	1990	9	AK098817 Homo sapi
32	1109.2	77.5	1631	9	AK097010 Homo sapi
33	1104.6	77.2	1465	10	S79307 Ig gamma =1
34	1103.6	77.1	1617	6	A29585 H.sapiens c
35	1102	77.0	1599	6	AX330501 Sequence
36	1102	77.0	1599	6	AX333307 Sequence
37	1102	77.0	1599	6	AX334122 Sequence
38	1102	77.0	1599	9	HUMIGHEPAH
39	1096.4	76.6	1633	9	AK097367 Homo sapi
40	1096	76.6	7521	6	AK080951 Sequence
41	1095.6	76.6	1549	6	A21385 Plasmid DNA
42	1092.6	76.4	6557	6	I26929 Sequence 3
43	1092.4	76.3	1666	9	BC006402 Homo sapi
44	1091.8	76.3	1341	6	A07562 DNA sequenc
45	1091.4	76.3	1639	9	AK097950 Homo sapi

ALIGNMENTS

RESULT 1	AR108863	Sequence 3	1431 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	AR108863	Sequence 3	from patent US 6113898.			
DEFINITION	AR108863					
ACCESSION	AR108863					
VERSION	AR108863.1	GI:12825139				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 1431)					
AUTHORS	Anderson, D.R., Brame, P., Hanna, N., Shestowsky, W.S. and Heard, C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	expressing said antibodies					
	Patent: US 6113898-A 3 05-SEP-2000;					

FEATURES		Location/Qualifiers			
source		1..1431			
BASE COUNT		/organism="unknown"			
ORIGIN		322 a 469 c 380 g 260 t			
Query Match		100.0%; Score 1431; DB 6; Length 1431;			
Best Local Similarity		100.0%; Pred. No. 4.6e-280;			
Matches 1431; Conservative		0; Mismatches 0; Indels 0; Gaps 0;			
Qy	1	ATGAACACCTGTGGTCTTCT			

Qy	961	CGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTACCGTCTCTCACCGTCTCTGCACCAG	1020
Db	961	CGGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTACCGTCTCTCACCGTCTCTGCACCAG	1020
Qy	1021	GACTGGCTGAATGGCAAGGAGTACAAAGTGAAGTCTCCAAACAAAGCCCTCCAGCCCC	1080
Db	1021	GACTGGCTGAATGGCAAGGAGTACAAAGTGAAGTCTCCAAACAAAGCCCTCCAGCCCC	1080
Qy	1081	ATCGAGAAAACCATCTCCAAAGCCAAAGGAGCCCGAGAGCCGAGAACCAAGGTGTACACCTG	1140
Db	1081	ATCGAGAAAACCATCTCCAAAGCCAAAGGAGCCCGAGAGCCGAGAACCAAGGTGTACACCTG	1140
Qy	1141	CCCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTCAGCTGCTGGTCAAGGC	1200
Db	1141	CCCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTCAGCTGCTGGTCAAGGC	1200
Qy	1201	TTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGACCCGAGAACCAACTAC	1260
Db	1201	TTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGACCCGAGAACCAACTAC	1260
Qy	1261	AAGACCAAGCCTCCCGTGGAGTCCGACGCTCTCTTCTCTACAGCAAGCTCAACC	1320
Db	1261	AAGACCAAGCCTCCCGTGGAGTCCGACGCTCTCTTCTCTACAGCAAGCTCAACC	1320
Qy	1321	GTGGACAAGAGCAGTGGCAGCAGGGGAACTCTTCTCATGCTCCGTGATGCAATGAGGCT	1380
Db	1321	GTGGACAAGAGCAGTGGCAGCAGGGGAACTCTTCTCATGCTCCGTGATGCAATGAGGCT	1380
Qy	1381	CTGCACAACTACTACAGCAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1431
Db	1381	CTGCACAACTACTACAGCAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1431
RESULT 2			
LOCUS	AR108867	1431 bp	DNA linear PAT 14-FEB-2001
DEFINITION	Sequence 11 from patent US 6113898.		
ACCESSION	AR108867		
VERSION	AR108867.1 GI:12825143		
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1431)		
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.		
TITLE	Human B7.1-specific primatized antibodies and transfectomas		
JOURNAL	expressing said antibodies		
FEATURES	Patent: US 6113898-A 11 05-SEP-2000;		
source	Location/Qualifiers		
BASE COUNT	319 a	462 c	385 g 265 t
ORIGIN	1. .1431		
	/organism="unknown"		
Query Match	91.9%;	Score 1315.8;	DB 6; Length 1431;
Best Local Similarity	95.0%;	Pred. NO. 1.1e-256;	
Matches 1359;	Conservative 0;	Mismatches 72;	Indels 0; Gaps 0;
Qy	1	ATGAACACCTGCTGGTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGGTCTCTGCCAG	60
Db	1	ATGAACACCTGCTGGTCTCTCCCTCCCTGGTGGGAGCTCCAGATGGGTCTCTGCCAG	60
Qy	61	GTGAAGCTGAGAGTGGGGGCAAGGACTTCTGCAGCTTCCGAGACCTGTCCCGGACC	120
Db	61	GTGCAGCTGAGAGTCCGGGCCAGAGACTTGGTGAAGCCTTCGAGAGCCCTGTCCCTCACC	120
Qy	121	TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTCTGGACCTGGATCCGCCAGACC	180
Db	121	TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC	180
Qy	181	CCAGGAGGGGAGCTGGAGTGGATTTGGCCATATTTATGGTAATGGTGCAGACCAACTAC	240

Db 181 CCAGGGAAGGCGCTGGAGTGGATTGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240
Qy 241 AATCCCTCCTCAAGAGTCGAGTCACCATTTCAAAGACACGTCCTCAAGAACACCATGTTCTTC 300
Db 241 AATCCCTCCTCAAGAGTCGAGTCACCATTTCAAAGACACGTCCTCAAGAACACCATGTTCTTC 300
Qy 301 CTGAAGCTTGAATCTGTGACCGACCGGACACGGCGCTTATTAATCTGTGCGAGAGCGCT 360
Db 301 CTGAAGCTTGAATCTGTGACCGCGCGGACACGGCGGTGTTACTGTGTGAGAGATCGT 360
Qy 361 CGCCCTGATGTGACCAACCATTTGTTATGGCGCTGGGTGCGATGTCTGGGGCCCGGGAGAC 420
Db 361 CTTTCTTTTCAGTTGTTGGAATGTTTACAAACACTGTTTCGATGTCTGGGGCCCGGGAGTC 420
Qy 421 CTGGTCACGCTCTCTCAGTAGACACCAAGGGCCCATCGGTCTTCCCTCTGGCAACCTGCC 480
Db 421 CTGGTCACGCTCTCTCAGTAGACACCAAGGGCCCATCGGTCTTCCCTCTGGCAACCTGCC 480
Qy 481 TCCAGAGACACCTCTGGGGGACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCC 540
Db 481 TCCAGAGACACCTCTGGGGGACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCC 540
Qy 541 GAACCGGTGACGGTGTCTGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCG 600
Db 541 GAACCGGTGACGGTGTCTGGAACTCAGCGCCCTGACAGCGGGGTGCACACCTTCCCG 600
Qy 601 GCTGCTCAGCTCTCAGGACTCTACTCTCCTCAGCAGCGTGGTGAACCGTCCAGC 660
Db 601 GCTGCTCAGCTCTCAGGACTCTACTCTCCTCAGCAGCGTGGTGAACCGTCCAGC 660
Qy 661 AGCTTGGGACCCAGACCTTACATCTGACGTAATCAAGCCCGGACGACCAAGGTC 720
Db 661 AGCTTGGGACCCAGACCTTACATCTGACGTAATCAAGCCCGGACGACCAAGGTC 720
Qy 721 GACAGAAAGCAGAGCCCAATCTTGTGACAAATCTCAGATGCGCCACCGTCCAGCA 780
Db 721 GACAGAAAGCAGAGCCCAATCTTGTGACAAATCTCAGATGCGCCACCGTCCAGCA 780
Qy 781 CTGAATCTCTGGGGGACCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
Db 781 CTGAATCTCTGGGGGACCGTCAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 840
Qy 841 ATGATCTCTCCGACCCCTGAGTCTACATGCTGCTGGTGGTGGAGCGTGAGCCACGACCT 900
Db 841 ATGATCTCTCCGACCCCTGAGTCTACATGCTGCTGGTGGTGGAGCGTGAGCCACGACCT 900
Qy 901 GAGGTCAAGTTCAAATGCTGACGCGCGTGGAGTGATTAATGCGCAAGCAAGCG 960
Db 901 GAGGTCAAGTTCAAATGCTGACGCGCGTGGAGTGATTAATGCGCAAGCAAGCG 960
Qy 961 CGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTGTGAGTCTTCAACCGTCTGACCCAG 1020
Db 961 CGGGAGGAGCAGTACAACAGCAGTACCGTGTGGTGTGAGTCTTCAACCGTCTGACCCAG 1020
Qy 1021 GACTGGTGAATGGCAGAGTACAAGTCAAGTCTCAACAAAGCCCTTCCAGCCGCC 1080
Db 1021 GACTGGTGAATGGCAGAGTACAAGTCTCAACAAAGCCCTTCCAGCCGCC 1080
Qy 1081 ATCGAGAAACCATCTTCAAAAGCCAAAGGCGAGCCCGGAGACCAAGTGTACACCTG 1140
Db 1081 ATCGAGAAACCATCTTCAAAAGCCAAAGGCGAGCCCGGAGACCAAGTGTACACCTG 1140
Qy 1141 CCCCCATCCCGGATGAGTGAACCAAGAACCAAGTCAGCTGACCTGCTGCTGCTCAAGGC 1200
Db 1141 CCCCCATCCCGGATGAGTGAACCAAGAACCAAGTCAGCTGACCTGCTGCTGCTCAAGGC 1200
Qy 1201 TTCTATCCAGGACATGCTCCCTGAGTGGAGAGCAATGGGCGAGCGGAGAACACTAC 1260
Db 1201 TTCTATCCAGGACATGCTCCCTGAGTGGAGAGCAATGGGCGAGCGGAGAACACTAC 1260
Qy 1261 AAGACACGCTCCCGTGTGACTCCGACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320
Db 1261 AAGACACGCTCCCGTGTGACTCCGACGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1320

Qy 1321 GTGGCAAGAGCAGGTGCGCAGCAGGGAAACGTTCTTCTCATGCTCGTGATGATGAGGT 1380
Db 1321 GTGGCAAGAGCAGGTGCGCAGCAGGGAAACGTTCTTCTCATGCTCGTGATGATGAGGT 1380
Qy 1381 CTGCAACACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1431
Db 1381 CTGCAACACCACTACACGACAGAGGCTCTCCCTGTCTCCGGGTAAATGA 1431
RESULT 3
E10697
LOCUS E10697 1431 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding heavy chain of human monoclonal antibody against human cytomegalovirus 65kD antigen.
ACCESSION E10697
VERSION E10697.1 GI:22027790
KEYWORDS JP 1996038178-A/20.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1431)
AUTHORS Tanaka, S., Niwa, H. and Tanaka, H.
TITLE HUMAN MONOCLONAL ANTIBODY AND PRODUCTION THEREOF, AND PRIMER FOR CLONING OF GENE THEREOF
JOURNAL Patent: JP 1996038178-A 20 13-FEB-1996;
COMMENT TANAKA HIDEYUKI, NISSHINO IND INC
OS Homo sapiens (human)
PN JP 1996038178-A/20
PD 13-FEB-1996
PF 20-FEB-1995 JP 1995030742
PR 18-FEB-1994 JP 94P 21628
PI TANAKA SHIGEKI, NIWA HIRONUKI, TANAKA HIDEYUKI PC
C12N15/09, C07K16/08, C12N1/21, C12N15/02, C12P21/08, C12Q1/68, PC
G01N33/53,
PC G01N33/531, G01N33/577, (C12N1/21, C12R1:19), (C12P21/08, PC
C12R1:19);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH key
FH source 1. .1431
FT /organism='Homo sapiens'
FT /cell_type='B cell',
FT sig_peptide 1. 57
FT /product='signal peptide of heavy chain of FT
human monoclonal
antibody against human cytomegalovirus 65kD
FT mat_peptide 58. 1425
FT /product='heavy chain of human monoclonal FT
antibody against
human cytomegalovirus 65kD antigen' FT CDS
FT 1. .1428
FT /product='heavy chain of human monoclonal FT
antibody against
human cytomegalovirus 65kD antigen' FT 3'UTR
FT 1429. >1431.
LOCATION/Qualifiers
1. .1431
/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 314 a 475 c 379 g 263 t
ORIGIN
FEATURES
source
Query Match 86.5%; Score 1237.2; DB 6; Length 1431;
Best Local Similarity 92.9%; Pred. No. 9, 1e-241;
Matches 1332; Conservative 0; Mismatches 93; Indels 9; Gaps 3;
Qy 1 ATGAAACACCTGTGGTCTTCTCTCTGTGGCAGCTCCAGATGGGTCTCTGTCTCCAG 60

[illegible]

361	AAATGGAAGTATCATGGGGACTGGTTCGACCCCTGGGGCCAAAGTACCACTGTACCGCTC	420
433	TCCTCAGCTAGCACAAAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCTCAAGAGCACC	492
421	TCCTCAGCTCCACCAAGGGCCCATCGGTCTTCCCTCCCTGGCACCTCTCTCAAGAGCACC	480
493	TCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACG	552
481	TCTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCGAACCGGTGACG	540
553	GTGTCGTGGAACTCAGCGGCCCTGACACAGCGGGGTGCACACCTTCCCGGTGCTCTACAG	612
541	GTGTCGTGGAACTCAGCGGCCCTGACACAGCGGGGTGCACACCTTCCCGGTGCTCTACAG	600
613	TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACACCTGCGCTCCAGCAGCTTGGGCACC	672
601	TCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACACCTGCGCTCCAGCAGCTTGGGCACC	660
673	CAGACTTACATCTGCAACGTTGAATCACAAGCCACGAACAACCAAGGTGGACAAGAAGCA	732
661	CAGACTTACATCTGCAACGTTGAATCACAAGCCACGAACAACCAAGGTGGACAAGAAGCA	720
733	GAGCCCAAACTTGTGACAAACTCAACATGCCCAACCGTCCAGCAGCACTGACTCTCTG	792
721	GAGCCCAAACTTGTGACAAACTCAACATGCCCAACCGTCCAGCAGCACTGACTCTCTG	780
793	GGGGGACCGTCAGCTTCTCTTCCCCCCCCCAAGCAACCCCAAGGACACCTCATGATCTCCCGG	852
781	GGGGGACCGTCAGCTTCTCTTCCCCCCCCCAAGCAACCCCAAGGACACCTCATGATCTCCCGG	840
853	ACCCCTGAGGTCAATCGTGGTGGACGTGAGCCACGAAGACCTCTGAGGTCAAGTTC	912
841	ACCCCTGAGGTCAATCGTGGTGGACGTGAGCCACGAAGACCTCTGAGGTCAAGTTC	900
913	AACGTGTACGTGGACGGGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAG	972
901	AACGTGTACGTGGACGGGTGGAGTGCATAATGCCAAGCAAAAGCCGCGGAGGAGCAG	960
973	TACAAACGACGTACCGGTGTGGTCAAGGCTCTCAACCGTCTGCAACAGGACTGGCTGAAT	1032
961	TACAAACGACGTACCGGTGTGGTCAAGGCTCTCAACCGTCTGCAACAGGACTGGCTGAAT	1020
1033	GGCAAGGAGTCAAGTGCAGAGTCTCAAACAAAGCCTTCCACGCCCATCGAGAAAACC	1092
1021	GGCAAGGAGTCAAGTGCAGAGTCTCAAACAAAGCCTTCCACGCCCATCGAGAAAACC	1080
1093	ATCTCCAAAGCCAAAGGACCCCGAGAACCAACAGGTGTACACCTTCCGCCCATCCCGG	1152
1081	ATCTCCAAAGCCAAAGGACCCCGAGAACCAACAGGTGTACACCTTCCGCCCATCCCGG	1140
1153	GATGAGCTGACAAAGAACCAAGTCCAGCTGCACCTGCTGGTCAAGGCTTCTATCCGAGC	1212
1141	GATGAGCTGACAAAGAACCAAGTCCAGCTGCACCTGCTGGTCAAGGCTTCTATCCGAGC	1200
1213	GACATCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACCACTACAAGACCAAGCCT	1272
1201	GACATCCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACCACTACAAGACCAAGCCT	1260
1273	CCCGTGTGACTCCGAGGCTCTCTTCTCTACAGCAAGCTCACCCTGGGACAAGAGC	1332
1261	CCCGTGTGACTCCGAGGCTCTCTTCTCTACAGCAAGCTCACCCTGGGACAAGAGC	1320
1333	AGTGGCAGCAGGGGAACGCTTCTCATGTCTCGTGTATGATGATGAGGCTCTGCAACAACAC	1392
1321	AGTGGCAGCAGGGGAACGCTTCTCATGTCTCGTGTATGATGATGAGGCTCTGCAACAACAC	1380
1393	TACACGACGAAGAGCCTCTCCCTGTCTCCCGGTAATG	1430
1381	TACACGACGAAGAGCCTCTCCCTGTCTCCCGGTAATG	1418

RESULT 7

AK057754

LOCUS AK057754 1594 bp mRNA linear PRI 27-MAR-2002
 DEFINITION Homo sapiens CDNA FLJ25025 fis, clone CBL01928, highly similar to
 IG gamma immunoglobulin heavy chain.
 ACCESSION AK057754 1 GI:16553681
 VERSION oligo capping; fis (full insert sequence).
 KEYWORDS Homo sapiens cerebellum cDNA to mRNA, clone_lib:CBL01928.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 Nishi, T., Nakagawa, S., Senoh, A., Mizuguchi, H., Inagaki, H.,
 Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M.,
 Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H.,
 Nishikawa, T., Sugiyama, A., Kawakami, B., Nagai, K., Isogai, T. and
 Sugano, S.
 NEDO human cDNA sequencing project
 TITLE UNPUBLISHED
 JOURNAL 2 (bases 1 to 1594)
 AUTHORS Sugano, S. and Suzuki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical Science,
 University of Tokyo, Laboratory of Genome Structure, Human Genome
 Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-1586,
 Fax:81-3-5449-5416)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of
 Economy, Trade and Industry of Japan; cDNA full insert sequencing:
 Research Association for Biotechnology (RAB); cDNA library
 construction and 5'-end one pass sequencing: Institute of Medical
 Science, University of Tokyo, Laboratory of Genome Structure, Human
 Genome Center; 3'-end one pass sequencing: RAB; clone selection for
 full insert sequencing: RAB and Helix Research Institute.
 FEATURES
 source
 1. 1594
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CBL01928"
 /tissue_type="cerebellum"
 /clone_lib="CBL"
 /notes="cloning vector: pME18SFL3"
 15. 1460
 /notes="unnamed protein product"
 /codon_start=1
 /protein_id="BAB71560.1"
 /db_xref="GI:16553682"
 /db_xref="IMG/LLGM:AK057754"
 /translations="MDVCKKKMKHFLFLLLVAAPRWLALQLQBSGPGGLVPRSETL
 TLTCSVSGDSIATGYFWMGFQPGKGLQFGISVYVYTAHNPSLKRVTISADTS
 KPAQFKTSTGAADTAVLYCARHWPRVLGVDFWDPMGPIGLTVSSASTKGPSVY
 FLAPSSKTSGGTAALGCLVKDYPRPVTWSNMGALTSGVHTFPVAVLOSGLYLSSS
 VVTPSSSLGTQFYI CNVNHKPSNTKDKVPEKSCDKHTCCPCPAPELLGGPSVFL
 FPPKDTLMISRTPEVKTCVVDVSHEDPEVKENWYDGVGEVHNHAKTKPREEQINSTY
 TNQVSLTCLVAGFYPSDAVEWESNGQPPENNYKTPPPVLVDSGDSFGFLYSKLIVDKSR
 WQQGNVFCSCVMHEALHNHYTKSLSLSPGK"
 BASE COUNT 338 a 532 c 437 g 287 t
 ORIGIN
 Query Match 84.9%; Score 1215.2; DB 9; Length 1594;
 Best Local Similarity 92.0%; Pred. No. 2.6e-236;
 Matches 1319; Conservative 0; Mismatches 103; Indels 12; Gaps 3;
 Qy 1 ATGAACACCTGGTCTTCTCCTCCTCGTGGCGAGCTCCAGATGGGTCTGTCCACG 60
 Db 36 ATGAACACCTGGTCTTCTCCTCCTCGTGGCGGCTCCAGATGGGTCTGTCCACG 95
 Qy 61 GTGAAGCTGCAGAGTGGGGCGAAGGACTTCTGCAGCTTCGGAGACCCCTGTCCCGCACC 120
 Db 96 TTGCAGCTGCAGAGTCCGGGCCAGGACTGGTGAAGCTTCGGAGACCTGACCTCAG 155
 Qy 121 TGCCTTCTCTCTGGTGGCTCCAT---CAGCGGTTACTACTACTGGA CTTGGATCCGCGAC 177

[illegible][illegible]

Db	540	CCCGAAACGGGTGACGGTGTCTGTGAACAATCAGGCGCCCTTGACCAGCGCGGTGACACACTTC	599	
Qy	598	CCGGCTGTCTTACAGTCTCTCAGGACTCTTAATCTCCCTCAGCACGCTGTGTGACCGTGCCTCTCC	657	
Db	600	CCGACTGTCTTACAGTCTCTCAGGACTCTAATCTCCCTCAGCAGCGTGTGTGACCGTGCCTCTCC	659	
Qy	658	AGCAGCTTTGGGCAACCCAGACCTTAATCTGTGCAACGTGAATCAGAAGCCAGCAACAACAAG	717	
Db	660	AGCAGCTTTGGGCAACCCAGACCTTAATCTGTGCAACGTGAATCAGAAGCCAGCAACAACAAG	719	
Qy	718	GTGACAAAGAAAGCAGAGCCCAATCTTGTGACAAAACCTCACAATGCCACCGTGCCTCA	777	
Db	720	GTGACAAAGAAAGTTGAGCCCAATCTTGTGACAAAACCTCACAATGCCACCGTGCCTCA	779	
Qy	778	GCACCTGAACTCTCGGGGGGACCGTCAAGTCTTCTCTTCCCCCAAACCAAGGACAC	837	
Db	780	GCACCTGAACTCTCGGGGGGACCGTCAAGTCTTCTCTTCCCCCAAACCAAGGACAC	839	
Qy	838	CTCATGATCTCCCGGACCCCTGAGGTCAATGCTGTGTGTGTGAGCGTGAGCCACGAGAC	897	
Db	840	CTCATGATCTCCCGGACCCCTGAGGTCAATGCTGTGTGTGTGAGCGTGAGCCACGAGAC	899	
Qy	898	CCTGAGTCAAGTTCAACTGCTAGCTGGAACCGGCGTGGAGTGCATAATGCCAACAAAG	957	
Db	900	CCTGAGTCAAGTTCAACTGCTAGCTGGAACCGGCGTGGAGTGCATAATGCCAACAAAG	959	
Qy	958	CCGCGGAGGAGCAGTAGTCAACAGCACCTTACCGTGTGTGTGTGAGCGTCTCAACCGTCTCTGCAC	1017	
Db	960	CCGCGGAGGAGCAGTAGTCAACAGCACCTTACCGTGTGTGTGTGAGCGTCTCAACCGTCTCTGCAC	1019	
Qy	1018	CAGGACTGGCTGAATGGCAAGGAGTCAAGTGCAGGTCTCCAACAAAGCCCTCCCAGCC	1077	
Db	1020	CAGGACTGGCTGAATGGCAAGGAGTCAAGTGCAGGTCTCCAACAAAGCCCTCCCAGCC	1079	
Qy	1078	CCCATCGAAAAACCATCTCCAAAGCCAAAGGGGAGCCCGCAGAACACAGGTGTATACAC	1137	
Db	1080	CCCATCGAAAAACCATCTCCAAAGCCAAAGGGGAGCCCGCAGAACACAGGTGTATACAC	1139	
Qy	1138	CTGCCCCCATCCCGGGATGAGCTGCACCAAGAACAGGTTCAGCTTCGCTTGGTCAAA	1197	
Db	1140	CTGCCCCCATCCCGGGATGAGCTGCACCAAGAACAGGTTCAGCTTCGCTTGGTCAAA	1199	
Qy	1198	GGCTTTCTATCCACGCGCATCGCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAACAC	1257	
Db	1200	GGCTTTCTATCCACGCGCATCGCCGTGGAGTGGGAGAGCAATGGCGAGCGGAGAACAC	1259	
Qy	1258	TACAAGACACCGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTTACAGCAGCTC	1317	
Db	1260	TACAAGACACCGCTCCCGTGTGAGCTCCGACGGCTCTTCTTCTCTTACAGCAGCTC	1319	
Qy	1318	ACCGTGGACAAGACAGGTGGCAGCGGGGAAACGTTCTCATGCTCCCGTATGCATGAG	1377	
Db	1320	ACCGTGGACAAGACAGGTGGCAGCGGGGAAACGTTCTCATGCTCCCGTATGCATGAG	1379	
Qy	1378	GCTCTGCACCAACCTACACGAGAAGCCCTCTCCCTGTCTCCGGGTAAATGA	1431	
Db	1380	GCTCTGCACCAACCTACACGAGAAGCCCTCTCCCTGTCTCCGGGTAAATGA	1433	
<hr/>				
RESULT 12				
AR135377				
LOCUS	AR135377	1404 bp	DNA	linear PAT 16-JUN-2001
DEFINITION	Sequence 11 from patent US 6136310.			
ACCESSION	AR135377			
VERSION	AR135377.1	GI:14476049		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1404)			
AUTHORS	Hanna.N., Newman,R.Anthoniy. and Reff,M.Elliott.			
TITLE	Recombinant anti-CD4 antibodies for human therapy			
JOURNAL	Patent: US 6136310-A 11 24-OCT-2000;			


```
Qy 1201 TTCTATCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCGAGCCGGAGAACAACTAC 1260
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1170 TTCTATCCAGCGACATCGCCGTGGAGTGGGAGCAATGGGCGAGCCGGAGAACAACTAC 1229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1261 AAGACCACGCTCCCGTGGTGGACTCGGACGGCTCCTTCTTCTCTACAGCAAGCTCACC 1320
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1230 AAGACCACACCTCCCAATGCTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACC 1289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1321 GTGGACAAGAGCAGGTGGGAGCAGGGGAACCTTCTCATGTCTCCGTGATGCATGAGGCT 1380
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1290 GTGGACAAGAGCAGGTGGGAGCAGGGGAACCTTCTCATGTCTCCGTGATGCATGAGGCT 1349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1381 CTGCACAACCACTACACGAGAGAGCCTTCTCCCTGTCTCCGGGTAAATGA 1431
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1350 CTGCACAACCACTACACGAGAGAGCCTTCTCCCTGTCTCCGGGTAAATGA 1400
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

Search completed: June 3, 2003, 17:50:48
Job time : 3719.97 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:15:24 ; Search time 1951.49 Seconds

(without alignments)
11875.950 Million cell updates/sec

Title: US-09-576-424-3

Perfect score: 1431

Sequence: 1 atgaacacctgtgtgtctt.....ccctgtctccgggtaaatga 1431

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hcc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hcc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_nam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	63.0	1020	14	BQ062878
2	864	60.4	947	14	BQ709771
3	850.4	59.4	958	14	BQ706140
4	842.4	58.9	926	12	BG755166
5	831.2	58.1	901	13	EM007892
6	830.4	58.0	988	14	BQ708857

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	824.4	57.6	1029	14	BQ063185	BQ063185	AGENCOURT
8	822.8	57.5	887	14	BQ711255	BQ711255	AGENCOURT
9	822.2	57.5	918	14	BQ708022	BQ708022	AGENCOURT
10	815.2	57.0	995	14	BM914540	BM914540	AGENCOURT
11	808.8	56.5	881	14	BQ711291	BQ711291	AGENCOURT
12	800.2	55.9	1031	14	BQ064886	BQ064886	AGENCOURT
13	797.4	55.7	936	14	BQ711727	BQ711727	AGENCOURT
14	796	55.6	940	14	BQ705928	BQ705928	AGENCOURT
15	787.4	55.0	977	14	BQ710532	BQ710532	AGENCOURT
16	786.4	55.0	980	14	BM914504	BM914504	AGENCOURT
17	785.2	54.9	843	13	BM007897	BM007897	603617582
18	778.8	54.4	991	14	BQ708936	BQ708936	AGENCOURT
19	777.2	54.3	973	14	BQ706204	BQ706204	AGENCOURT
20	772.6	54.0	930	13	BM007597	BM007597	603616995
21	770.6	53.9	981	14	BM914528	BM914528	AGENCOURT
22	764.6	53.4	926	14	BQ710304	BQ710304	AGENCOURT
23	764.2	53.4	917	14	BQ708169	BQ708169	AGENCOURT
24	759.4	53.1	961	14	BQ710233	BQ710233	AGENCOURT
25	756.6	52.9	945	14	BQ712403	BQ712403	AGENCOURT
26	752.4	52.6	1012	14	BM914556	BM914556	AGENCOURT
27	750.4	52.4	783	13	BM007838	BM007838	603617519
28	750.2	52.4	895	14	BQ708303	BQ708303	AGENCOURT
29	748	52.3	1026	14	BM914288	BM914288	AGENCOURT
30	741.4	51.8	914	14	BQ712363	BQ712363	AGENCOURT
31	738	51.6	913	14	BQ707472	BQ707472	AGENCOURT
32	733.8	51.3	944	14	BQ712397	BQ712397	AGENCOURT
33	733.6	51.3	919	14	BQ709339	BQ709339	AGENCOURT
34	732.8	51.2	936	14	BQ707530	BQ707530	AGENCOURT
35	732.6	51.2	906	14	BQ711709	BQ711709	AGENCOURT
36	731.8	51.1	1014	14	BM914505	BM914505	AGENCOURT
37	730.4	51.0	973	14	BQ708902	BQ708902	AGENCOURT
38	729.6	51.0	888	12	BG757604	BG757604	602714780
39	728.8	50.9	941	14	BQ712021	BQ712021	AGENCOURT
40	728.6	50.9	925	14	BQ709853	BQ709853	AGENCOURT
41	728.4	50.9	991	14	BQ707621	BQ707621	AGENCOURT
42	727.6	50.8	855	13	BM007689	BM007689	603617119
43	726.8	50.8	870	12	BG757815	BG757815	602711335
44	726.2	50.7	925	14	BQ709152	BQ709152	AGENCOURT
45	725.8	50.7	923	14	BQ881523	BQ881523	AGENCOURT

ALIGNMENTS

RESULT 1
BQ062878
LOCUS BQ062878 1020 bp mRNA linear EST 02-APR-2002
DEFINITION AGENCOURT_6826949 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924420
5', mRNA sequence.
ACCESSION BQ062878
VERSION BQ062878.1 GI:19890085
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1020)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LCM2094 row: h column: 21
High quality sequence start: 21
High quality sequence stop: 681.
Location/Qualifiers


```
source 1. .1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924420"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 239 a 344 c 269 g 166 t 2 others
ORIGIN
Query Match 63.0%; Score 902; DB 14; Length 1020;
Best Local Similarity 98.0%; Pred. No. 1.1e-204;
Matches 923; Conservative 0; Mismatches 17; Indels 2; Gaps 1;
QY 489 CACCTCTGGGGGACAGCGCGCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGT 548
Db |||||
36 CACCTCTGGGGGACAGCGCGCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGT 95
QY 549 GACGGTGTCTGGAACCTCAGGCGCCTGACAGCGCGTGCACACCTTCCCGGCTGCTCT 608
Db |||||
96 GACGGTGTCTGGAACCTCAGGCGCCTGACAGCGCGTGCACACCTTCCCGGCTGCTCT 155
QY 609 ACAGTCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGG 668
Db |||||
156 ACAGTCTCAGGACTTACTCTCTCAGCAGCGTGTGACCGTGCCTCCAGCAGCTTGGG 215
QY 669 CACCCAGACTACCTGCAAGTGAATCAAGCCCGAGCAACCAAGGTTGGAAGAA 728
Db |||||
216 CACCCAGACTACCTGCAAGTGAATCAAGCCCGAGCAACCAAGGTTGGAAGAA 275
QY 729 AGCAGAGCCCAATCTGTGACAAACTCACATGCTCCACCGTGCCTCCAGCAGCTTGG 788
Db |||||
276 AGTTAGCCCAATCTGTGACAAACTCACATGCTCCACCGTGCCTCCAGCAGCTTGG 335
QY 789 CTGGGGGACCGTCACTCTCTCTTCCCGGACCAAGGACCGCTCATGATCTC 848
Db |||||
336 CTGGGGGACCGTCACTCTCTCTTCCCGGACCAAGGACCGCTCATGATCTC 395
QY 849 CCGGACCCCTGAGTCAATGCTGTGTGACGTCGACGTCGACGTCGACGTCGACGTC 908
Db |||||
396 CCGGACCCCTGAGTCAATGCTGTGTGACGTCGACGTCGACGTCGACGTCGACGTC 455
QY 909 GTTCAACTGCTGACGCGGTGAGTGCATATGCAAGCAAGCAAGCAAGCAAGCAAG 968
Db |||||
456 GTTCAACTGCTGACGCGGTGAGTGCATATGCAAGCAAGCAAGCAAGCAAGCAAG 515
QY 969 GCAGTCAACAGCAGTACCGTGTGTGTCAGCGTCTCACCCTGCTGACGAGCTGGCT 1028
Db |||||
516 GCAGTCAACAGCAGTACCGTGTGTGTCAGCGTCTCACCCTGCTGACGAGCTGGCT 575
QY 1029 GAATGGCAAGGATCAAGTCAAGTCTTCAAGCAAGCCCTCCAGCGCCCATCGAGAA 1088
Db |||||
576 GAATGGCAAGGATCAAGTCAAGTCTTCAAGCAAGCCCTCCAGCGCCCATCGAGAA 635
QY 1089 AACCATCTCAAGGCAAGGAGCGCCCGAGAACCAAGGTCACCCCTGCGCCCATC 1148
Db |||||
636 AACCATCTCAAGGCAAGGAGCGCCCGAGAACCAAGGTCACCCCTGCGCCCATC 695
QY 1149 CCGGATGAGCTGACCAAGAACCAAGTCAAGCTGCTGCTGTGTCAGAGGCTTCTATCC 1208
Db |||||
696 CCGGATGAGCTGACCAAGAACCAAGTCAAGCTGCTGCTGTGTCAGAGGCTTCTATCC 755
QY 1209 CAGCCATCTGCGCTGAGTGGAGCAATGGGAGCGCGA--GAACAACTACAAGACC 1266
Db |||||

Db 756 CAGCGACATCGCCGTGGAGTGGAGAGCAATGGGAGCGCGGNAGAAAATCTACTACTAGACC 815
QY 1267 AGCGCTCCCGTGTGCTGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTACCGTGGAC 1326
Db |||||
816 AGCGCTCNGTGTGCTGACTCCGACGGCTCTCTTCTCTTACAGCAAGCTACCGTGGGA 875
QY 1327 AAGAGCAGGTGGCAGCAGCGGGAACGTCTTCTCATGCTCCGTGATCATGAGCTCTGCAC 1386
Db |||||
876 CAGAGCAGGTGGCAGCAGCGGGAACGTCTTCTCATGCTCCGTGATCATGAGCTCTGCAC 935
QY 1387 AACCACTACAGCAGCAAGAGCTCTCTCTGTCTCCGGGTAAA 1428
Db |||||
936 AACCACTACAGCAGCAAGAGCTCTCTCTGTCTCCGGGTAAA 977

RESULT 2
BQ709771 947 bp mRNA linear EST 16-JUL-2002
LOCUS AGENCOURT_8353965 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278583
DEFINITION 5', mRNA sequence.
ACCESSION BQ709771
VERSION BQ709771.1 GI:21848670
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloning by: Agencourt Bioscience Corporation
Cloning distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LUCM2466 row: m column: 16
High quality sequence start: 3
High quality sequence stop: 675.
FEATURES
Location/Qualifiers
1. .947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6278583"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 225 a 320 c 252 g 150 t
ORIGIN
Query Match 60.4%; Score 864; DB 14; Length 947;
Best Local Similarity 99.4%; Pred. No. 1.2e-195;
Matches 867; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 560 GGAACTCAGGCGCCTGACCAAGCGCGTGCACACTTCCCGCTGTCTCAGTCTCAG 619
Db |||||
9 GAACTCAGGCGCCTGACCAAGCGCGTGCACACTTCCCGCTGTCTCAGTCTCAG 68
QY 620 GACTCTACTCTCAGCAGCGTGTGACCGTCCCGCTCCAGCGCTTGGGACCCAGACT 679
Db |||||
69 GACTCTACTCTCAGCAGCGTGTGACCGTCCCGCTCCAGCGCTTGGGACCCAGACT 128
```


QY 680 ACATCTGCAACGTGAATCAACAGCCAGCAACACCAAGGTGGACAGAAAGACAGACCCCA 739
 Db 129 ACATCTGCAACGTGAATCAACAGCCAGCAACACCAAGGTGGACAGAAAGTTGAGCCCA 188
 QY 740 AATCTTGTGCAAAACTCACATGTCCTCCCGTCCAGCAGCCTGAACTCTCTGGGGGAC 799
 Db 189 AATCTTGTGCAAAACTCACATGTCCTCCCGTCCAGCAGCCTGAACTCTCTGGGGGAC 248
 QY 800 CGTCACT 859
 Db 249 CGTCACT 308
 QY 860 AGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 919
 Db 309 AGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 368
 QY 920 ACTGTGACGCGGTGGAGGTGCTAATGCTCAAGCAAGCGCGGGAGGAGCAGTCAACA 979
 Db 369 ACTGTGACGCGGTGGAGGTGCTAATGCTCAAGCAAGCGCGGGAGGAGCAGTCAACA 428
 QY 980 GCACGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1039
 Db 429 GCACGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 488
 QY 1040 AGTCAAGTGCAGGTCTCAACAAAGCCCTCCAGCAGCCCTCCAGCAGCCCTCCAGCAG 1099
 Db 489 AGTCAAGTGCAGGTCTCAACAAAGCCCTCCAGCAGCCCTCCAGCAGCCCTCCAGCAG 548
 QY 1100 AAGCCAAAGGCGAGCGCCAGACACACAGGTGACACCTGCTGCTGCTGCTGCTGCTGCT 1159
 Db 549 AAGCCAAAGGCGAGCGCCAGACACACAGGTGACACCTGCTGCTGCTGCTGCTGCTGCT 608
 QY 1160 TGACCAAGAACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219
 Db 609 TGACCAAGAACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 668
 QY 1220 CCGTGAAGTGGAGAGCAATGGGAGCGGAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1279
 Db 669 CCGTGAAGTGGAGAGCAATGGGAGCGGAGAGCAATGCTGCTGCTGCTGCTGCTGCTGCT 728
 QY 1280 TGGACTCCGAGCGCT 1339
 Db 729 TGGACTCCGAGCGCT 788
 QY 1340 AGCAGGAGCAAGCT 1399
 Db 789 AGCAGGAGCAAGCT 848
 QY 1400 AGAAGAGCT 1431
 Db 849 AGAAGAGCT 880

RESULT 3

BQ706140

LOCUS

BQ706140 958 bp mRNA linear EST 16-JUL-2002

AGENCY: NCBI

5', mRNA sequence.

ACCESSION

BQ706140

VERSION

BQ706140.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 958)

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Straube, Ph.D.

Email: csapbs-f@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LCM2464 row: a column: 01
 High quality sequence stop: 705.

Location/Qualifiers
 1..958

FEATURES

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6277512"

/clone_lib="NIH_MGC_113"

/lab_host="DH10B (phage-resistant)"

/note="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:

ECORI; cDNA made by oligo-dT priming. Directionally cloned

into EORI/XhoI sites using the following 5' adaptor:

GGCAGAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH_MGC Library."

BASE COUNT 229 a 319 c 256 g 150 t 4 others

ORIGIN

Query Match

Best Local Similarity 59.4%; Score 850.4; DB 14; Length 958;

Matches 865; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 558 GTGAGTCACTGAGCGGCTGACAGCGGGGTGACACACCTTCCCGGTGCTCAGAGCTCTC 617

Db 11 GTGAGTCACTGAGCGGCTGACAGCGGGGTGACACACCTTCCCGGTGCTCAGAGCTCTC 70

QY 618 AGGACTCTACT 677

Db 71 AGGACTCTACT 130

QY 678 CTACATCTGCAACGTGAATCAACAGCCAGCAACCAAGGTGGACAGAAAGACAGAGCC 737

Db 131 CTACATCTGCAACGTGAATCAACAGCCAGCAACCAAGGTGGACAGAAAGTTGAGCC 190

QY 738 CAATCTTTGTGCAAAACTCACATGCTCCAGCGTCCAGCAGCCTGAGACTCTCTGGGGG 797

Db 191 CAATCTTTGTGCAAAACTCACATGCTCCAGCGTCCAGCAGCCTGAGACTCTCTGGGGG 250

QY 798 ACCGTGAGTCT 857

Db 251 ACCGTGAGTCT 310

QY 858 TGAGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917

Db 311 TGAGGTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 370

QY 918 GTACGTGAGCGGCTGAGGTGCTGATATGCTCAAGCAAAAGCGCGGAGAGCAGTACAA 977

Db 371 GTACGTGAGCGGCTGAGGTGCTGATATGCTCAAGCAAAAGCGCGGAGAGCAGTACAA 430

QY 978 CAGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1037

Db 431 CAGCAGTACCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490

QY 1038 GGAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTTCCAGCGCCCTCCAGCAAAACCAATCTC 1097

Db 491 GGAGTACAAAGTCAAGGTCTCCAAACAAAGCCCTTCCAGCGCCCTCCAGCAAAACCAATCTC 550

QY 1098 CAAAGCAAAAGGCGAGCGCCCGAGAGACCAAGGTGTACACCTGCCCCCCTATCCCGGATGA 1157

Db 551 CAAAGCAAAAGGCGAGCGCCCGAGAGACCAAGGTGTACACCTGCCCCCCTATCCCGGATGA 610

QY 1158 GCTGACCAAGAACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1217

Db 611 GCTGACCAAGAACCAAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 670


```

QY 453 CCATCGTCTTCCCTCGGACCTCTCTCCAAAGACACCTCTGGGGGACAGCGGCCCT 512
Db 65 CCATCGTCTTCCCTCGGACCTCTCTCCAAAGACACCTCTGGGGGACAGCGGCCCT 124
QY 513 GGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGAGGTCTCGTGAATCATGAGCG 572
Db 125 GGGTGCCTGGTCAAGGACTACTTCCCGAACCGGTGAGGTCTCGTGAATCATGAGCG 184
QY 573 CTGTACACAGCGGCGTGCACACCTTCCCGGTCTCTTACAGTCTCTCAGGACTCTACTCCCT 632
Db 185 CTGTACACAGCGGCGTGCACACCTTCCCGGTCTCTTACAGTCTCTCAGGACTCTACTCCCT 244
QY 633 CAGCAGCGTGTGACCGTGCCTTCAGCAGTGTGGGACCCAGACCTACATCTGCAAGCT 692
Db 245 CAGCAGCGTGTGACCGTGCCTTCAGCAGTGTGGGACCCAGACCTACATCTGCAAGCT 304
QY 693 GAATCAGAGCCCGACCAACCAAGGTGACAGAAAGCAGAGCCCAATCTTGTGACAA 752
Db 305 GAATCAGAGCCCGACCAACCAAGGTGACAGAAAGTGTAGCCCAATCTTGTGACAA 364
QY 753 AACTCAGACATGCCACCGTCCAGCAGCTGAACCTCTTGGGGGACCGTCACTTCTCT 812
Db 365 AACTCAGACATGCCACCGTCCAGCAGCTGAACCTCTTGGGGGACCGTCACTTCTCT 424
QY 813 CTTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGT 872
Db 425 CTTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGT 484
QY 873 GGTGGTGGACGTGAGCCAGAGACCTTCAAGTCAAGTTCACTGTAGTGGACGGGT 932
Db 485 GGTGGTGGACGTGAGCCAGAGACCTTCAAGTCAAGTTCACTGTAGTGGACGGGT 544
QY 933 GGAGGTGATCAATATGCCAAGCAAAAGCGCGGAGGAGAGTCAACAGCAGCAGTACCCTGT 992
Db 545 GGAGGTGATCAATATGCCAAGCAAAAGCGCGGAGGAGGAGTCAACAGCAGCAGTACCCTGT 604
QY 993 GGTGAGCGTCTTACCGTCTTGACAGACTGGTGAATGAGAGGAGTCAAGTGCAA 1052
Db 605 GGTGAGCGTCTTACCGTCTTGACAGACTGGTGAATGAGAGGAGTCAAGTGCAA 664
QY 1053 GGTCTCCAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGCA 1112
Db 665 GGTCTCCAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGCA 724
QY 1113 GCCCGGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTCAACCAAGAACCA 1172
Db 725 GCCCGGAGAACACAGGTGTACACCTGCCCCCATCCCGGATGAGTCAACCAAGAACCA 783
QY 1173 GGTGAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATGCGCGTGGAGTGGGA 1232
Db 784 GGTGAGCTGACCTGCTGGTCAAGGCTTCTATCCAGCGACATGCGCGTGGAGTGGGA 843
QY 1233 GAGCAATGGGAG-CGGGAGAACACTACAGACCAAGCAGCGCTCCCGT---CTGGACTCG 1288
Db 844 GAGCAATGGGAGCGCGGAGAACACTACAGACCAAGCAGCGCTCCCGGCTCGGAACTCG 903
QY 1289 ACGGC-TCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGCAGCGGTGGGAGCA 1343
Db 904 ACGGCTTCTTCTTCTCTACAGAAAGCTCCCGGGGAGCAAGCAGCGGTGGCA 959

RESULT 7
LOCUS BQ0631185
DEFINITION AGENCOURT_687667 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5924769
5', mRNA sequence.
ACCESSION BQ0631185
VERSION BQ0631185.1 GI:19890681
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 1029)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2095 row: g column: 10
High quality sequence stop: 723.
Location/Qualifiers

FEATURES
source

1..1029
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5924769"
/clone_lib="NIH_MGC_99"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pORF7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 237 a 350 c 276 g 165 t 1 others
ORIGIN

Query Match 57.6%; Score 824.4; DB 14; Length 1029;
Best Local Similarity 99.0%; Pred. No. 3.7e-186;
Matches 861; Conservative 0; Mismatches 6; Indels 3; Gaps 3;

```

QY 483 CAAGAGCACCCTCGGGGACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGA 542
Db 4 CAAGAGCACCCTCGGGGACAGCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGA 63
QY 543 ACCGCTGACGGTGTCTGGAACTCAGCGCCCTCGACCGCGGTGCACACCTTCCCGGC 602
Db 64 ACCGCTGACGGTGTCTGGAACTCAGCGCCCTCGACCGCGGTGCACACCTTCCCGGC 123
QY 603 TGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAG 662
Db 124 TGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAGCAG 183
QY 663 CTGGGCAACCCAGACCTACATCTGCAACGTGAATCACAAGCCCGACCAACCAAGGTGGA 722
Db 184 CTGGGCAACCCAGACCTACATCTGCAACGTGAATCACAAGCCCGACCAACCAAGGTGGA 243
QY 723 CAAGAAACAGACGCCCAATCTTGTGACAAACTCACAATGCCCGTCCCGACGACC 782
Db 244 CAAGAAAGTTCAGCCCAATCTTGTGACAAACTCACAATGCCCGTCCCGACGACC 303
QY 783 TGAATCTCTGGGGGACCGGTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 842
Db 304 TGAATCTCTGGGGGACCGGTGAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 363
QY 843 GATCTCCCGGACCCCTGAGGTGACATGCGTGTGTGGACCGTGGCCAGGACCCCTCA 902
Db 364 GATCTCCCGGACCCCTGAGGTGACATGCGTGTGTGGACCGTGGCCAGGACCCCTCA 423
QY 903 GGTCAAGTTCAACTGTTACGTGGAGCGGTGGAGGTGCATATGCAAGACCAAGCCCGG 962
Db 424 GGTCAAGTTCAACTGTTACGTGGAGCGGTGGAGGTGCATATGCAAGACCAAGCCCGG 483
QY 963 GGAGGAGCAGTACAAACAGCAAGTACCGGTGTGTGAGTCTCTTCAAGTCTTGCACAGGA 1022

```

Db 484 GGAGGAGCAGTACACAGCAGTACCGTGTGGTGTGAGCGTCTCACCCTGTCACACGGA 543
Qy 1023 CTGGCTGAATGCAAGAGTCAAGTCAAGGTCTCCAAAGAGCCCTCCACAGCCCAT 1082
Db 544 CTGGCTGAATGCAAGAGTCAAGTCAAGGTCTCCAAAGAGCCCTCCACAGCCCAT 603
Qy 1083 CGAGAAACCATCTCCAAAGCAAGAGGAGCCCGAGAACCAACAGGTGTACACCCCTGCC 1142
Db 604 CGAGAAACCATCTCCAAAGCAAGAGGAGCCCGAGAACCAACAGGTGTACACCCCTGCC 663
Qy 1143 CCCATCCCGGATGAGTCTGACCAAGAACCCAGGTGAGCTGCTGCTGCTCAAGGGCTT 1202
Db 664 CCCATCCCGGATGAGTCTGACCAAGAACCCAGGTGAGCTGCTGCTGCTCAAGGGCTT 723
Qy 1203 CTATCCAGCGACATCGCGGTGGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAA 1262
Db 724 CTATCCAGCGACATCGCGGTGGAGTGGAGAGCAATGGGAGCGGAGAACCACTACAA 783
Qy 1263 GACACGCGCT-CCCGTGTGAGTCTCGAGCGGTCTCTTCTCTTACA-GCAGGTACCC 1320
Db 784 GAACACGCGCTCCCGTGTGAGTCTCGAGCGGTCTCTTCTCTTACAGGCAAGTCAAC 843
Qy 1321 GTGGACAAGACA-GGTGGCAGCAGGGAA 1349
Db 844 GTGGACCAAGCAGGAGTGGCAGCAGGGGA 873

RESULT 8
LOCUS B0711255
DEFINITION AGENCOURT_8443471 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6281659
5', mRNA sequence.
ACCESSION B0711255
VERSION B0711255.1 GI:21850154
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 887)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLM2474 row: m column: 20
High quality sequence stop: 681.
Location/Qualifiers
1. .887
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6281659"
/clone_lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
source

BASE COUNT 218 a 295 c 230 g 143 t 1 others
ORIGIN
Query Match 57.5%; Score 822.8; DB 14; Length 887;

Best Local Similarity 97.6%; Pred. No. 8.3e-186;
Matches 866; Conservative 0; Mismatches 18; Indels 3; Gaps 3;
Qy 541 GAAACCGGTGACGGTGTCTGTGGAATCTCAGGCGCCCTGACAGCGGCGTGCACACCTTCCCG 600
Db 1 GAAACCGGTGACGGTGTCTGTGGAATCTCAGGCGCCCTGACAGCGGCGTGCACACCTTCCCG 60
Qy 601 GCTGTCTTACAGTCTCTCAGGACTCTCTCTCTCAGAGCGTGTGACCGTGCCTCCAGC 660
Db 61 GCTGTCTTACAGTCTCTCAGGACTCTCTCTCTCAGAGCGTGTGACCGTGCCTCCAGC 120
Qy 661 AGCTTGGGCAACCCAGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720
Db 121 AGCTTGGGCAACCCAGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Qy 721 GACAAAGAGCAGAGCCCAAAATCTTGTGCAAAAATCTACATGCCCCACCGTGCCTCCAGCA 780
Db 181 GACAAAGAGTGTGAGCCCAAAATCTTGTGCAAAAATCTACATGCCCCACCGTGCCTCCAGCA 240
Qy 781 CCTGAATCTCTGGGGGACCGTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 241 CCTGAATCTCTGGGGGACCGTCAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Qy 841 ATGATCTCTCCGAGCCCTGAGGTCAATGCGTGTGGTGTGGAGCTGAGCCAGCAAGACCT 900
Db 301 ATGATCTCTCCGAGCCCTGAGGTCAATGCGTGTGGTGTGGAGCTGAGCCAGCAAGACCT 360
Qy 901 GAGGTCAAGTTCACCTGCTGAGCGGCTGAGGTGTCATATGCCCCAAGACCAAGCCG 960
Db 361 GAGGTCAAGTTCACCTGCTGAGCGGCTGAGGTGTCATATGCCCCAAGACCAAGCCG 420
Qy 961 CGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTGTGGAGCTCTCTCTCTCTCTCTCTCT 1020
Db 421 CGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTGTGGAGCTCTCTCTCTCTCTCTCTCT 480
Qy 1021 GACTGGCTGAATGGCAGAGGTACAAAGTGTCAAGTGTCTCAACAAAGCCCTCCAGCCCT 1080
Db 481 GACTGGCTGAATGGCAGAGGTACAAAGTGTCAAGTGTCTCAACAAAGCCCTCCAGCCCT 540
Qy 1081 ATCGAGAAACCATCTCCAAAGCAAGGCGAGCCCGAGAACCAACACAGGTGTACACCTCTG 1140
Db 541 ATCGAGAAACCATCTCCAAAGCAAGGCGAGCCCGAGAACCAACACAGGTGTACACCTCTG 600
Qy 1141 CCCCCATCCCGGATGAGTGTGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 1200
Db 601 CCCCCATCCCGGATGAGTGTGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 660
Qy 1201 TTCTATCCAGGACATCGCGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGT 1260
Db 661 TTCTATCCAGGACATCGCGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGT 720
Qy 1261 AAGA-CCACGCTCCCGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 1319
Db 721 NAGACCCAGCTCCCGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 780
Qy 1320 CGT-GGACAAAGCAGGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 1377
Db 781 CGTGGACAAAGCAAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGGAGTGTGG 840
Qy 1378 GCTGTGCAACCACTTACACGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1424
Db 841 GCTGTGCAACCACTTACACGAGAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 887

RESULT 9
B0708022
LOCUS B0708022
DEFINITION AGENCOURT_8353641 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6279643
5', mRNA sequence.
ACCESSION B0708022
VERSION B0708022.1 GI:21846921
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 918)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM2469 row: i column: 20
High quality sequence stop: 667.
Location/Qualifiers
1..918
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279643"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH-MGC Library."
BASE COUNT 208 a 316 c 245 g 147 t 2 others
ORIGIN
Query Match 57.5%; Score 822.2; DB 14; Length 918;
Best Local Similarity 95.4%; Pred. No. 1.2e-185;
Matches 867; Conservative 0; Mismatches 40; Indels 2; Gaps 2;
QY 398 TCGATGTCGGGGCCGGGAGACCTGGTCCACCTGCTCTCAGCTAGCACCAGGCGCCAT 457
DB 1 TTGACCGTGTGGGGCCGAGGAAACGCTGGTCAACCTGCTCTCAGCCCTCCACCAAGGCGCCAT 60
QY 458 CGGTCTTCCCTCGCACCTCTCTCAAGAGCACTCTGGGGGACAGCGCCCTGGGCT 517
DB 61 CGGTCTTCCCTCGCACCTCTCTCAAGAGCACTCTGGGGGACAGCGCCCTGGGCT 120
QY 518 GCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGGAACTCAGGCGCCCTGA 577
DB 121 GCCTGGTCAAGGACTACTTCCCGGAACCGGTGACGGTGTCTGGGAACTCAGGCGCCCTGA 180
QY 578 CCAGGGGGTGACACCTTCCCGGTGTCTCAGTCTCAGGACTTACTCCCTCAGCA 637
DB 181 CCAGGGGGTGACACCTTCCCGGTGTCTCAGTCTCAGGACTTACTCCCTCAGCA 240
QY 638 GGGTGTGACCGTCCCTCCAGCAGCTGGGACCCAGCACTTACATCTGCAACGTGAATC 697
DB 241 GGGTGTGACCGTCCCTCCAGCAGCTGGGACCCAGCACTTACATCTGCAACGTGAATC 300
QY 698 ACAAGCCGACGACACCAAGGTGGACAGAAAGAGAGCCCAAAATCTTGTGACAAAATC 757
DB 301 ACAAGCCGACGACACCAAGGTGGACAGAAAGTTGAGCCCAAAATCTTGTGACAAAATC 360
QY 758 ACACATGCCCGGCGCCAGACCTGAATCTCTGGGGGACCGTCACTTCTCTTCC 817
DB 361 ACACATGCCCGGCGCCAGACCTGAATCTCTGGGGGACCGTCACTTCTCTTCC 420
QY 818 CCCCACCAACCAAGACACCTTCATGATCTCCCGGACCCCTCAGTCTCAGTCTCGGTGG 877
DB 421 CCCCACCAACCAAGACACCTTCATGATCTCCCGGACCCCTCAGTCTCAGTCTCGGTGG 480
QY 878 JGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAGTGTGACGTGGACGCGGTGGAGG 937

Db 481 TGGACGTGAGCCAGAAAGACCCTGAGGTCAAGTTCAACTGTGACGCGCGTGGAGG 540
QY 938 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGCCTGACGTTGGTCA 997
Db 541 TGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAGCCTGACGTTGGTCA 600
QY 998 GCGTCCTCACCGTCTCTGCACCAAGGACTGGCTGGAATGGCAAGAGGTACAAGTGAAGTCT 1057
Db 601 GCGTCCTCACCGTCTCTGCACCAAGGACTGGCTGGAATGGCAAGAGGTACAAGTGAAGTCT 660
QY 1058 CCACAAAGCCCTCCAGCCCGCCCATTCGAGAAAAACATCTCCAAAGCCAAAGGAGCGCC 1117
Db 661 CCACAAAGCCCTCCAGCCCGCCCATTCGAGAAAAACATCTCCAAAGCCAAAGGAGCGCC 720
QY 1118 GAGAACCAACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGTCAACCAAGAACCAAGTCA 1177
Db 721 GAGAACCAACAGGTGTACACCCCTGCCCCCATCCCGGGATGAGTCAACCAAGAACCAAGTCA 780
QY 1178 GCCTGACCTGCTGCTCAAAAGCTTCTATCCAGCGACATCGCCGT-GGAGTGGGAGAGC 1236
Db 781 GCCTGACCTGCTGCTCAAAAGCTTCTATCCAGCGACATCNCGNGGGAGTGGGAGAGC 840
QY 1237 AATGGGAG-CCGAGAACAACTACAGACCAACCGCTCCCGTCTGGACTCGGAGGCTC 1295
Db 841 ATGGGGAGCCCGGAGAACAACTACAGACCAACCGCTCCCGGCTGGGACTCCCGACGG 900
QY 1296 CTTCTTCTCT 1304
Db 901 GTCCTTCTCT 909
RESULT 10
LOCUS BM914540 995 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6615506 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480223
5', mRNA sequence.
ACCESSION BM914540
VERSION BM914540.1 GI:19364919
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 995)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM2002 row: 1 column: 16
High quality sequence stop: 718.
Location/Qualifiers
1..995
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5480223"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
source

BASE COUNT 241 a 330 c 259 g 165 t
ORIGIN NIH_MGC Library, "
Query Match 57.0%; Score 815.2; DB 14; Length 995;
Best Local Similarity 96.1%; Pred. No. 5.7e-184;
Matches 857; Conservative 0; Mismatches 33; Indels 2; Gaps 2;
QY 393 CTGGGTGATGTCCTGGGGCCCGGAGACCTGGTGACCGTCTCTCAGTAGACCAAGGG 452
DB |||||
6 CTACTTTGACGATGGGGCCGAGGACGCTGGTCAACCGTCTCTCAGCTCCACCAAGGG 65
QY 453 CCCATCGGTCTTCCCGCTGGACACCTCTCCAGAGCACCTCTGGGGGACACGCGCCT 512
DB |||||
66 CCATCGGTCTTCCCGCTGGACACCTCTCCAGAGCACCTCTGGGGGACACGCGCCT 125
QY 513 GGGCTGCTGTGTCAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAATCTCAGGCGC 572
DB |||||
126 GGGCTGCTGTGTCAGGACTACTTCCCGAACCGGTGACGGTGTGCTGGAATCTCAGGCGC 185
QY 573 CTGACGACGCGGTGACACCTTCCCGCTGTCTTACAGTCTCTCAGGACTCTACTCCCT 632
DB |||||
186 CTTGACGACGCGGTGACACCTTCCCGCTGTCTTACAGTCTCTCAGGACTCTACTCCCT 245
QY 633 CAGCAGCGGTGACCGTCCCTCCAGCAGCTTGGGCAACCTACATCTGCAAGCT 592
DB |||||
246 CAGCAGCGGTGACCGTCCCTCCAGCAGCTTGGGCAACCTACATCTGCAAGCT 305
QY 693 GAATCACAAGCCGAGCAACCAAGGTGCAAGAAAGCAGAGCCCAAACTTTGTGACAA 752
DB |||||
306 GAATCACAAGCCGAGCAACCAAGGTGCAAGAAAGTTGAGCCCAAACTTTGTGACAA 365
QY 753 AACTCACAATGCCAAGCCGAGCAACCTGAACTCTTGGGGGACCGTCACTTCTCT 812
DB |||||
366 AACTCACAATGCCAAGCCGAGCAACCTGAACTCTTGGGGGACCGTCACTTCTCT 425
QY 813 CTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGTCACTAGCT 872
DB |||||
426 CTTCCCCCAAAACCCAGGACACCTCATGATCTCCCGGACCCCTGAGTCACTAGCT 485
QY 873 GGTGTGGACGTGAGCCAGGACACCTGAGGTCAAGTTCAACTGTGTAGTGGAGCGGT 932
DB |||||
486 GGTGTGGACGTGAGCCAGGACACCTGAGGTCAAGTTCAACTGTGTAGTGGAGCGGT 545
QY 933 GGAGTGCATATGCAAGCAAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGT 992
DB |||||
546 GGAGTGCATATGCAAGCAAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGT 605
QY 993 GGTGACGTCTTCCCGTCTGACAGGACCTGAGTGAATGCAAGGAGTACAGTGCA 1052
DB |||||
606 GGTGACGTCTTCCCGTCTGACAGGACCTGAGTGAATGCAAGGAGTACAGTGCA 665
QY 1053 GGTCTTCCAAAGCCCTCCAGCCCAATCGAGAAACCACTCCAAAGCCAAAGGCA 1112
DB |||||
666 GGTCTTCCAAAGCCCTCCAGCCCAATCGAGAAACCACTCCAAAGCCAAAGGCA 725
QY 1113 GCCCCGAGAACCAAGGTGTACACCTTCCCGGATGAGTGCACCAAGAACCA 1172
DB |||||
726 GCCCCGAGAACCAAGGTGTACACCTTCCCGGATGAGTGCACCAAGAACCA 785
QY 1173 GGTGACGTGACCTGCTGGTCAAGGCTTCTATCCGAGGACATGCGGTGAGTGGG- 1231
DB |||||
786 GGTGACGTGACCTGCTGGTCAAGGCTTCTATCCAGGACTTCCCGGAGTGGGA 845
QY 1232 AGAGCAATGGGAGCGGAGAACAACTACAAGA-CCAGCCTCCCGTCTGG 1282
DB |||||
846 AAGCAATGGGAGCGGAGAACAACTACAAGACCCCGCCTCCCGTCTGG 897

RESULT 11
B0711291 881 bp mRNA linear EST 16-JUL-2002
LOCUS B0711291 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6279096
DEFINITION AGENCOURT_8347186 NIH_MGC_113 Homo sapiens cdna clone IMAGE:6279096

5', mRNA sequence.
B0711291 GI:21850190
VERSION B0711291.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM2468 row: c column: 01
High quality sequence stop: 721.
Location/Qualifiers
1. 881
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6279096"
/clone.lib="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ScoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
BASE COUNT 220 a 285 c 237 g 139 t
ORIGIN

Query Match 56.5%; Score 808.8; DB 14; Length 881;
Best Local Similarity 99.8%; Pred. No. 1.8e-182;
Matches 810; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 612 GTCTTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGAC 671
DB |||||
1 GTCTTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTCCCTCCAGCAGCTTGGGAC 60
QY 672 CCAGACCTTACATCTGCAACGTTGAATCAACAGCCCAACCAAGGTGGACAAAGGC 731
DB |||||
61 CCAGACCTTACATCTGCAACGTTGAATCAACAGCCCAACCAAGGTGGACAAAGAGT 120
QY 732 AGAGCCCAATCTTGTGACAAACTCACAATGCCACCGTCCCGGACCACTGACTCT 791
DB |||||
121 TGAGCCCAATCTTGTGACAAACTCACAATGCCACCGTCCCGGACCACTGACTCT 180
QY 792 GGGGGGACCGTCAGTCTTCTTCCCGGACCAACCAAGGACACCTCATCATCTCCCG 851
DB |||||
181 GGGGGGACCGTCAGTCTTCTTCCCGGACCAACCAAGGACACCTCATCATCTCCCG 240
QY 852 GACCCCTCAGGTACATCGTGGTGGTGGAGCGTGAGCCACCAAGACCCCTGAGGTCAAGTT 911
DB |||||
241 GACCCCTCAGGTACATCGTGGTGGTGGAGCGTGAGCCACCAAGACCCCTGAGGTCAAGTT 300
QY 912 CAATGTTAGTGGACCGCGTGGAGTGCATATGCAAGCAAAAGCCCGGAGGAGCA 971
DB |||||
301 CAATGTTAGTGGACCGCGTGGAGTGCATATGCAAGCAAAAGCCCGGAGGAGCA 360
QY 972 GTACAAAGCAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1031
DB |||||
361 GTACAAAGCAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 420

ACCESSION BQ711727
 VERSION BQ711727.1 GI:21850626
 EST.
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 936)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2518 row: k column: 18
 High quality sequence stop: 547.
 Location/Qualifiers
 1..936
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6301961"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 231 a 306 c 245 g 152 t 2 others
 BASE COUNT
 ORIGIN
 Query Match 55.7%; Score 797.4; DB 14; Length 936;
 Best Local Similarity 98.3%; Pred. No. 9.9e-180;
 Matches 926; Conservative 0; Mismatches 12; Indels 2; Gaps 2;
 QY 593 CTTTCCCGCTCTCTACAGTCTCTCAGGACTTACTCTCCTCAGCAGCGTGTGACCGTGC 652
 DB 10 CTTTCCCGCTCTCTACAGTCTCTCAGGACTTACTCTCCTCAGCAGCGTGTGACCGTGC 69
 QY 653 CTTCAGCAGCTTGGGCCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAACA 712
 DB 70 CTTCCAGCAGCTTGGGCCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAACA 129
 QY 713 CCAAGTGGACAAGAAGCAGAGCCCAATCTTGTGACAAACTCACAATGCCACCGT 772
 DB 130 CCAAGTGGACAAGAAGTGTGAGCCCAATCTTGTGACAAACTCACAATGCCACCGT 189
 QY 773 GCCCAGCAGCTGAATCTCTGGGGGACCGTCACTTCTTCTCCCGCCCAAAACCCAAAG 832
 DB 190 GCCCAGCAGCTGAATCTCTGGGGGACCGTCACTTCTTCTCCCGCCCAAAACCCAAAG 249
 QY 833 ACACCTCTATGATCTCCCGGACCCCTGAGGTACATGCTGTGTGGTGGAGCGTGAAGCAG 892
 DB 250 ACACCTCTATGATCTCCCGGACCCCTGAGGTACATGCTGTGTGGTGGAGCGTGAAGCAG 309
 QY 893 AGAGCCCTGAGTCAAGTTCACTGTAGCTGAGCGCGTGGAGTGCATATGCCAAGA 952
 DB 310 AGAGCCCTGAGTCAAGTTCACTGTAGCTGAGCGCGTGGAGTGCATATGCCAAGA 369
 QY 953 CAAAGCCCGGAGGAGCAGTACAAACAGCAGCTACCGTGTGTGCTCAGCGTCTCAGCGTCC 1012
 DB 370 CAAAGCCCGGAGGAGCAGTACAAACAGCAGCTACCGTGTGTGCTCAGCGTCTCAGCGTCC 429
 QY 1013 TGCACCAAGGACTGGCTGAATGGCAAGGAGTACAAGTGAAGGTCTCCAAAGAGCCCTCC 1072

Db 430 TGCACCAAGGACTGGCTGAATGGCAAGGAGTACAGTGAAGGTCTCCAAAGAGCCCTCC 489
 QY 1073 CAGCCCCCATCGAGAAAACCATCTTCAAGCAAAAGGCGAGCCCGAGAAACACAGGTGT 1132
 Db 490 CAGCCCCCATCGAGAAAACCATCTTCAAGCAAAAGGCGAGCCCGAGAAACACAGGTGT 549
 QY 1133 ACACCTCTCCCGGATCGAGTGCAGCCAGAACCAAGGTCAGCTGACCTGCCTCGCTGG 1192
 Db 550 ACACCTCTCCCGGATCGAGTGCAGCCAGAACCAAGGTCAGCTGACCTGCCTCGCTGG 609
 QY 1193 TCAAGAGGCTTCTATCCAGCGACATCGCGCTGGAGTGGAGAGCAATGGCGAGCCGAGA 1252
 Db 610 TCAAGAGGCTTCTATCCAGCGACATCGCGCTGGAGTGGAGAGCAATGGCGAGCCGAGA 669
 QY 1253 ACAACTACAAGACCA-CGCTTCCGCTGTGAGCTCCGAGCGTCTTCTTCTCTTACAGC 1311
 Db 670 ACAACTACNAGAACACCGCTCCGCTGTGAGCTCCGAGCGCTCTTCTTCTCTTACAGC 729
 QY 1312 AAGCTCACCGTGGACAAAGAGCAGTGGCGAGCGGGAACGTTCTCATGCTCCGCTGATG 1371
 Db 730 AAGCTCACCGTGGACAAAGAGCAGTGGCGAGCGGGAACGTTCTCATGCTCCGCGATG 789
 QY 1372 CATGAGGCTCTGCACAACCACTACACGAGCAAGAGCCCTCTCCTCTCTCCGGGTAAATGA 1431
 Db 790 CATGAGGCTCTGGAC-ACACTTAACCCGAGAGAGCCCTCTTCTGTCTCCCGGAATGA 848
 RESULT 14
 LOCUS BQ705928 940 bp mRNA linear EST 16-JUL-2002
 DEFINITION AGENCOURT_7976186 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6214795
 5', mRNA sequence.
 ACCESSION BQ705928
 VERSION BQ705928.1 GI:21844827
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 940)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 cDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCM2382 row: k column: 20
 High quality sequence stop: 619.
 Location/Qualifiers
 1..940
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6214795"
 /clone_lib="NIH_MGC_113"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Library constructed by Ling Hong in the
 Laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."
 235 a 318 c 240 g 147 t
 BASE COUNT
 ORIGIN

FEATURES
source

Query Match 55.6%; Score 796; DB 14; Length 940;
Best Local Similarity 99.3%; Pred. No. 2.1e-179;
Matches 810; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 617 CAGGACTCTACTCCCTCAGCAGCGTGGTACCGCTCCCTCAGCAGCTTGGGCAACCAG 676
Db 1 CAGGACTCTACTCCCTCAGCAGCGTGGTACCGCTCCCTCAGCAGCTTGGGCAACCAG 60
QY 677 CTTACATCTGCAACGTGAATCAACGCCAGCAACCAAGAGTGGACAAGAAAGCAGAGC 736
Db 61 CTTACATCTGCAACGTGAATCAACGCCAGCAACCAAGAGTGGACAAGAAAGTGGAGC 120
QY 737 CCAAAATCTTGTGCAAAATCAACATGCCCCCAAGGACACCCCTCATGATCTCCCGGACCC 856
Db 121 CCAAAATCTTGTGCAAAATCAACATGCCCCCAAGGACACCCCTCATGATCTCCCGGACCC 240
QY 797 GACCGTCAGTCTTCTCTTCCCTCCCAAGGACACCCCTCATGATCTCCCGGACCC 856
Db 181 GACCGTCAGTCTTCTCTTCCCTCCCAAGGACACCCCTCATGATCTCCCGGACCC 240
QY 857 CTGAGTGCATGCGTGGTGGAGCGTGAGGCAAGAGCCCTGAGGTCAAGTTCAACT 916
Db 241 CTGAGTGCATGCGTGGTGGAGCGTGAGGCAAGAGCCCTGAGGTCAAGTTCAACT 300
QY 917 GGTACGTGACGCGTGGAGTGCATAATGCCAAGCAAGCCGCGGGAGGAGCAGTACA 976
Db 301 GGTACGTGACGCGTGGAGTGCATAATGCCAAGCAAGCCGCGGGAGGAGCAGTACA 360
QY 977 ACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1036
Db 361 ACAGCAGTACCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
QY 1037 AGGAGTACAAAGTGAAGTGTCCAAAGAGCCCTCCAGCCCTCCATCGAGAAACCACT 1096
Db 421 AGGAGTACAAAGTGAAGTGTCCAAAGAGCCCTCCAGCCCTCCATCGAGAAACCACT 480
QY 1097 CAAAGCCAAAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1156
Db 481 CAAAGCCAAAGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 1157 AGCTGACCAAGAACCAAGGTCAGCTGACCTGGTCAAGAGCTTCTATCCAGCGACA 1216
Db 541 AGCTGACCAAGAACCAAGGTCAGCTGACCTGGTCAAGAGCTTCTATCCAGCGACA 600
QY 1217 TCGCGGTGAGTGGAGAGCAATGGCAGCGGAGCAAACTACAAGACCAAGCCCTCCCG 1276
Db 601 TCGCGGTGAGTGGAGAGCAATGGCAGCGGAGCAAACTACAAGACCAAGCCCTCCCG 660
QY 1277 TGCTGGACTCCGACCGCTCTTCTTCTCTACAGCAGCTACCGTGGAGCAAGCAGGT 1336
Db 661 TGCTGGACTCCGACCGCTCTTCTTCTCTACAGCAGCTACCGTGGAGCAAGCAGGT 720
QY 1337 GGCAGCAGGGGAACCTTCTCTCATGCTCGGTGATGATGAGGCTCTGACAAACCACTACA 1396
Db 721 GGCAGCAGGGGAACCTTCTCTCATGCTCGGTGATGATGAGGCTCTGACAAACCACTACA 780
QY 1397 CGC-AGAAGAGCTTCCCTGTCTCCGGTAAATGA 1431
Db 781 CGCAAAAGAGAGCTCTCCCTGTCTCCCGTAAATGA 816

RESULT 15
BQ710532
LOCUS
DEFINITION AGENCOURT_8352211 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277538
5', mRNA sequence.
ACCESSION BQ710532
VERSION BQ710532.1 GI:21849431
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 977)
NIH-MGC <http://mgc.mci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCW2464 row: b column: 03
High quality sequence stop: 749.
Location/Qualifiers
1. 977
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6277538"
/lab_host="NIH MGC 113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen, Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

FEATURES
source

BASE COUNT 227 a 331 c 264 g 154 t 1 others
ORIGIN
Query Match 55.0%; Score 787.4; DB 14; Length 977;
Best Local Similarity 92.5%; Pred. No. 2.4e-177;
Matches 886; Conservative 0; Mismatches 57; Indels 15; Gaps 5;
QY 475 CCCTCTCTCAAGAGCAGCCTCTGGGGGACAGCGGCCCTGGGTGCTGGTCAAGGACTAC 534
Db 11 CCCTCTCTCAAGAGCAGCCTCTGGGGGACAGCGGCCCTGGGTGCTGGTCAAGGACTAC 70
QY 535 TTCCCGGACCGGTGACGGTGTCTGGAACTCAGCGGCCCTTGACAGCGGGTGACACC 594
Db 71 TTCCCGGACCGGTGACGGTGTCTGGAACTCAGCGGCCCTTGACAGCGGGTGACACC 130
QY 595 TTCCCGGCTGCTACAGTCTCTAGGACTCTCTCCCTCAGCAGCGTGGTCAACCGTCCC 654
Db 131 TTCCCGGCTGCTACAGTCTCTAGGACTCTCTCCCTCAGCAGCGTGGTCAACCGTCCC 190
QY 655 TCCAGCAGCTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAACACC 714
Db 191 TCCAGCACTTGGGACCCAGACCTACATCTGCAACGTGAATCAAGCCCGAGCAACACC 250
QY 715 AAGTGACAAAGAAAGCAGAGCCCAAAATCTTGTGACAAAATCTACAATGCCACCGTGC 774
Db 251 AAGTGACAAAGAAAGCAGAGCCCAAAATCTTGTGACAAAATCTACAATGCCACCGTGC 301
QY 775 CCAGCAGTGAATCTCTGGGGGACCGTCACTCTCTCTTCCCGCCCAAAACCAAGGAC 834
Db 302 CCAGCAGTGAATCTCTGGGGGACCGTCACTCTCTTCTCTCTCTCTCTCTCTCTCTCT 358
QY 835 ACCCTCATGATCTCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCGAGCCAGCA 894
Db 359 ACCCTCATGATCTCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCGAGCCAGCA 418
QY 895 GACCTGAGGTCAAGTTCAACTGTGACGCGCGTGGAGGTGCATTAATGCCAAGACA 954
Db 419 GACCTGAGGTCAAGTTCAACTGTGACGCGCGTGGAGGTGCATTAATGCCAAGACA 478
QY 955 AAGCCGGGGAGGAGCAGTACAACAGCAGCTACCGTGGTGGTGGTGGTGGTGGTGGTGG 1014
Db 479 AAGCCGGGGAGGAGCAGTACAACAGCAGCTACCGTGGTGGTGGTGGTGGTGGTGGTGG 538

Qy	1015	CAC	CAG	A	G	A	C	T	G	G	T	G	A	A	T	G	G	A	A	G	G	A	G	T	C	A	A	G	A	A	G	C	C	T	C	C	A	1074														
Db	539	CAC	CAG	A	C	T	G	A	C	T	G	G	T	G	A	A	T	G	C	A	A	G	A	G	T	C	C	A	A	G	A	A	G	C	C	T	C	C	A	598												
Qy	1075	G	C	C	C	C	A	T	C	C	A	A	G	C	C	A	A	G	G	G	C	A	G	C	C	C	C	A	A	G	A	A	C	A	C	A	G	T	G	T	A	1134										
Db	599	G	C	C	C	C	A	T	C	C	A	A	G	C	C	A	A	G	G	G	C	A	G	C	C	C	C	A	A	G	A	A	C	A	C	A	G	T	G	T	A	658										
Qy	1135	A	C	C	T	G	C	C	C	C	A	T	C	C	C	G	G	A	T	G	A	C	T	G	A	C	C	T	G	A	C	C	T	G	A	C	T	G	C	T	G	T	C	1194								
Db	659	A	C	C	T	G	C	C	C	C	A	T	C	C	C	G	G	A	G	A	T	G	A	C	C	T	G	A	C	C	T	G	A	C	C	T	G	C	T	G	T	C	718									
Qy	1195	A	A	G	G	C	T	T	C	A	T	C	C	C	A	G	C	G	A	C	A	T	C	-	G	C	G	T	G	A	G	A	G	C	A	A	T	G	G	G	A	1253										
Db	719	A	A	G	G	C	T	T	C	A	T	C	C	C	C	A	G	C	G	A	C	A	T	C	T	C	C	G	T	G	A	G	A	A	T	G	G	G	A	C	G	G	A	778								
Qy	1254	C	A	A	C	T	A	A	G	A	C	A	C	G	C	T	C	C	G	T	G	T	G	A	C	T	C	C	G	A	G	C	T	C	T	T	C	T	C	T	A	C	A	G	C	A	1313					
Db	779	C	A	A	C	T	A	N	C	A	G	C	A	C	T	C	C	A	T	G	C	T	G	A	C	T	C	C	A	G	C	G	G	C	T	T	T	C	T	C	T	A	C	A	G	-	A	837				
Qy	1314	G	C	T	C	A	C	C	G	T	G	G	A	C	A	G	A	G	T	G	G	C	A	G	C	A	G	G	G	A	A	C	T	T	C	T	C	A	T	G	C	T	C	C	G	T	A	G	C	A	1373	
Db	838	G	C	T	C	A	C	C	G	T	G	G	A	C	A	G	A	A	G	T	G	G	C	A	G	C	A	G	G	G	A	A	C	T	T	C	T	C	A	T	G	C	T	C	C	G	T	A	G	C	A	897
Qy	1374	T	G	A	G	G	T	C	T	G	C	A	A	C	A	C	T	A	C	G	C	A	A	G	A	G	A	G	A	G	A	G	C	T	C	C	C	T	G	T	C	C	G	G	T	A	A	A	T	A	1431	
Db	898	T	G	A	G	G	T	C	T	G	C	C	C	A	C	C	C	T	A	C	A	C	A	-	A	A	G	A	G	C	T	C	C	T	G	T	C	T	G	T	C	G	G	T	A	A	A	T	A	954		

Search completed: June 3, 2003, 19:28:15
Job time : 1955.49 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 319.784 Seconds
(without alignments)
10077.457 Million cell updates/sec

Title: US-09-576-424-3
Perfect score: 1431
Sequence: 1 atgaacacctgtggtttt.....ccctgtctccgggtaaatga 1431

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SID32/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID32/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID32/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID32/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID32/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID32/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID32/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID32/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID32/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID32/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
11: /SID32/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
12: /SID32/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
13: /SID32/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
14: /SID32/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
15: /SID32/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
16: /SID32/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
17: /SID32/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
18: /SID32/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
19: /SID32/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
20: /SID32/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
21: /SID32/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
22: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
23: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID32/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	18 AAT62510	Primatized anti-hu
2	1431	100.0	1431	19 AAV35485	Macaque primatized
3	1431	100.0	1431	24 AAT517243	DNA sequence of a
4	1315.8	91.9	1431	18 AAT62513	Primatized anti-hu
5	1315.8	91.9	1431	19 AAV35489	Macaque primatized
6	1315.8	91.9	1431	24 AAT517247	DNA sequence of a
7	1246.4	87.1	1634	21 AAZ50012	Human immune syste
8	1237.2	86.5	1431	17 AAT18059	Monoclonal antibody
9	1234.8	86.3	1567	22 AAC66522	Human immune syste

10	1221.6	85.4	1418	17 AAT26889	Anti-rhesus D reco
11	1171.4	81.9	1404	18 AAT62868	Human gamma-4 heav
12	1168.2	81.6	1404	18 AAT62870	Human gamma-4pe hea
13	1166.6	81.5	1404	18 AAT62869	Human gamma-4G hea
14	1135	79.3	1428	22 AAT74680	Nucleotide sequenc
15	1125.2	78.6	1428	18 AAT61241	Human anti-RSV mon
16	1124.2	78.6	1507	21 AAO09695	Human immunoglobul
17	1122.8	78.5	1430	24 AAK98701	cDNA of the heavy
18	1117.2	78.1	1437	19 AAV35487	Macaque primatized
19	1117.2	78.1	1437	24 AAT17245	DNA sequence of a
20	1115.6	78.0	1437	18 AAT13847	Primatized anti-hu
21	1115.4	77.9	1442	22 AAC84208	Plasmid Glambda-1B
22	1113.4	77.8	1798	21 AAC98220	Human colon cancer
23	1113.2	77.8	1644	22 AAS22593	Human CDNA encodin
24	1112.8	77.8	19035	19 AAV61794	Traget plasmid Man
25	1112.2	77.7	6281	22 AAC84206	Plasmid Glambda-1A
26	1110.8	77.6	1428	18 AAT61279	Human anti-RSV mon
27	1103.6	77.1	1617	13 AAQ35099	Antibody D heavy c
28	1103	77.1	1467	14 AAQ23570	Reshaped CAMPATH-1
29	1102	77.0	1599	24 ABK64550	Human benign prost
30	1102	77.0	1599	24 ABL62673	Colon adenocarcino
31	1102	77.0	1599	24 ABL65479	Lung cancer relate
32	1102	77.0	1599	24 ABL66294	Lung cancer relate
33	1100.8	76.9	1427	19 AAV41429	Plasmid Hu19Hcpod
34	1100.8	76.9	1427	19 AAV41431	Plasmid Hu19Hcpod
35	1098.8	76.8	1449	20 AAX08951	Monoclonal antibod
36	1098.8	76.8	1449	20 AAX06952	Monoclonal antibod
37	1097.6	76.7	1427	19 AAV41432	Plasmid Hu19Hcpod
38	1096.6	76.6	1612	22 AAS22482	Human CDNA encodin
39	1096	76.6	7521	22 AAF30315	Bicistronic chimer
40	1094	76.5	1549	13 AAQ20066	Encodes heavy chai
41	1093.8	76.4	1458	13 AAQ23571	Reshaped CD4 antib
42	1093.8	76.4	1458	13 AAQ23581	Reshaped CD4 antib
43	1092.8	76.4	6284	19 AAV41427	Plasmid Hu19Hcpod
44	1092.6	76.4	6557	17 AAT15932	Anti-IgE VH expres
45	1092.2	76.3	1617	24 AAS62784	cDNA sequence #571

ALIGNMENTS

RESULT 1
AAT62510
ID AAT62510 standard; DNA; 1431 BP.
XX
AC AAT62510;
XX
DT 25-MAY-1997 (first entry)
XX
DE Primatized anti-human B7.1 antigen antibody 7C10 heavy chain DNA.
XX
KW Monoclonal antibody; cynomolgus monkey; macaque; 7C10;
KW Primatized antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma; ss.
XX
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
XX
PN WO9640878-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US10053.
XX
PR 07-JUN-1995; 95US-0487550.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
XX Anderson DR, Brams P, Hanna N, Shestowsky WS;
XX

Db 78 ATGAAACATCTGTGTTCTTCTTCTCTGTTGGCAGCTCCAGATGGTCTGTGCCAG 137
Qy 61 GTGAAGCTGCAGAGTGGGGGAAAGGACTTCTGACAGCCTTCGGAGACCCCTGTCCGACCC 120
Db 138 GTGAGCTGCAGAGTGGGGCCAGGACTGGTGAAGCCTTCGGAGACCCCTGTCCCTACC 197
Qy 121 TCGCTGTCTGTGGTGTCCATCAGCGGTACTACTGACCTGTGATCGCCAGACCC 180
Db 198 TGCATGTCTGTGGTGTCCATCAGGAGT---TACTACTGGAAGTGGTCCGGTGGCC 254
Qy 181 CCAGGAGGAGCTGAGTGGATTCGCCATATTTATGTTAATGTTGTCGACCAACCACTAC 240
Db 255 CCAGGAGGAGCTGAGTGGATTCGGTATATCTA---TACTAGTGGGAGCAACCACTAC 311
Qy 241 AATCCCTCCCTCAAGAGTGCAGTACCAATTTCAAAGACACGTCCTCAAGAACCACTTCTTC 300
Db 312 AACCCCTCCCTCAAGAGTGCAGTACCAATTCAGTAGACAGTCCCAAGAACCACTTCTTC 371
Qy 301 CTGAATCTGAATCTGTGACCGACCGGACAGCGCCGTCTATTACTGTGCGAGAGGCCCT 360
Db 372 CTGAAGCTGAGCTGTGTGACCGCTCGGACACCGCCGTGTATTACTGTGCGAGACCCCGG 431
Qy 361 CGCCCTGATTGCACAACTTTGTTATGGCGCTGGTCTGATGTTCTGGGGC-CCGGAGA 419
Db 432 CCCAAGCTACTACTACTA-----CGGTATGGACTTCTGGGGCCCAAGGAGC 478
Qy 420 CTTGTCTACCGCTCTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTC 479
Db 479 CTTGTCTACCGCTCTCTCAGCTCTCACCAAGGGCCCATCGGTCTTCCCGCTGGCACCCCTC 538
Qy 480 TCCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGCTCAAGGACTACTTCCC 539
Db 539 TCCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCGTGCTCAAGGACTACTTCCC 598
Qy 540 CGAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACCGGGGTGTCACACCTTCCC 599
Db 599 CGAACCGGTGACGGTGTGTGAACTCAGGCGCCCTGACCGGGGTGTCACACCTTCCC 658
Qy 600 GGCTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAG 659
Db 659 GGCTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTCCCTCCAG 718
Qy 660 CAGCTTGGGACCCAGACTCATCTGCAACGTGAATCAAGCCAGCAACCAAGGT 719
Db 719 CAGCTTGGGACCCAGACTCATCTGCAACGTGAATCAAGCCAGCAACCAAGGT 778
Qy 720 GGACAAGAACGACAGCCCAATCTGTGACAAACTCACATGCCACCGTGGCCAGC 779
Db 779 GGACAAGAACGACAGCCCAATCTGTGACAAACTCACATGCCACCGTGGCCAGC 838
Qy 780 ACCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCT 839
Db 839 ACCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCCCAAAACCAAGGACACCT 898
Qy 840 CATGATCTCCCGACCCCTGAGGTCAATCGTGTGTGGTGGACGTGAGCCAGCAAGACCC 899
Db 899 CATGATCTCCCGACCCCTGAGGTCAATCGTGTGTGGTGGACGTGAGCCAGCAAGACCC 958
Qy 900 TGAGTCAAGTTCACACTGGTAGTGGACCGGTGAGGTGCATTAATGCCAGCAAAAGCC 959
Db 959 TGAGTCAAGTTCACACTGGTAGTGGACCGGTGAGGTGCATTAATGCCAGCAAAAGCC 1018
Qy 960 GCGGAGGAGCAGTACACAGCACCTTACCGTGTGTGTCAGCGTCTCACCGTCTCCACCA 1019
Db 1019 GCGGAGGAGCAGTACACAGCACCTTACCGTGTGTGTCAGCGTCTCACCGTCTCCACCA 1078
Qy 1020 GGAATGGCTGAATGGCAAGGAGTACAGGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCC 1079
Db 1079 GGAATGGCTGAATGGCAAGGAGTACAGGTCAAGGTCTCCAAAGAGCCCTCCAGCCGCC 1138
Qy 1080 CATCAGAAACCATCTCCAAAGCCAAAGGGAGCCCGCGAGAACCAAGGTGTACACCT 1139

Db 1139 CATCAGAAACCATCTCCAAAGCCAAAGGAGCGCCCGAGAACCAAGTGTACACCT 1198
Qy 1140 GCGCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTCCCTGGTCAAAGG 1199
Db 1199 GCGCCCATCCCGGATGAGCTGACCAAGAACCAAGTCAAGCTGACCTCCCTGGTCAAAGG 1258
Qy 1200 CTTCTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGGACCGGAGAACCACTA 1259
Db 1259 CTTCTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGGACCGGAGAACCACTA 1318
Qy 1260 CAAGACCAAGCTCCCGTGGTGGACTCCGACGGGTCTTCTTCTTCTTACAGCAAGCTAC 1319
Db 1319 CAAGACCAAGCTCCCGTGGTGGACTCCGACGGGTCTTCTTCTTCTTACAGCAAGCTAC 1378
Qy 1320 CGTGCAAGAGCAGGTGGCAGCGGGAACGTCTTCTCATGCTCCGTCATGATGATGAGGC 1379
Db 1379 CGTGCAAGAGCAGGTGGCAGCGGGAACGTCTTCTCATGCTCCGTCATGATGATGAGGC 1438
Qy 1380 TCTGCACAACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1431
Db 1439 TCTGCACAACTACACGAGAGAGCTCTCCCTGTCTCCGGTAAATGA 1490

RESULT 8

AAT18059

ID AAT18059 standard; DNA; 1431 BP.

AC AAT18059;

XX AAT18059;

DT 16-AUG-1996 (first entry)

XX 16-AUG-1996 (first entry)

DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.

KW Polymerase chain reaction; primer; PCR; light chain; Mab;

KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis; ss.

XX Synthetic.

XX Synthetic.

XX Synthetic.

XX Synthetic.

FH Key Location/Qualifiers

FT CDS 1..1428

FT sig_peptide /tag= a

FT mat_peptide /tag= b

FT 3'UTR 58..1425

FT 1426..1431

FT /tag= c

FT /tag= d

XX JP08038178-A.

XX 13-FEB-1996.

XX 20-FEB-1995; 95JP-0030742.

XX 18-FEB-1994; 94JP-0021628.

XX (NISN) NISSHINO IND INC.

XX (TANA/) TANAKA H.

XX WPI; 1996-154852/16.

XX P-PSDB; AAR93553.

XX Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -

XX produced by primer amplification, used in the diagnosis of hCMV

XX infection

XX Claim 6; Page 16-18; 22pp; Japanese.

XX The sequences given in AAT18059-60 encode the heavy and light chains

XX respectively of a monoclonal antibody against a 65 kD antigen of human

XX cytomegalovirus (hCMV). These sequences were amplified using the

XX sequences given in AAT18040-58. The monoclonal antibody may be used

XX in the diagnosis of hCMV.

PA	(INSP) INST PASTEUR.
XX	(PROT-) PROTEINE PERFORMANCE.
XX	
PI	Chaabihi H, Edelman L, Kaczorek M, Margaratte C;
XX	
DR	WPI; 1996-162018/17.
DR	P-PSDB; AAR931166.
XX	
PT	Recombinant anti-rhesus D monoclonal antibody - expressed by
PT	baculovirus-transformed insect cells and useful for preventing
PT	haemolysis in new-born babies
XX	
PS	Claim 1; Page 35-37; 46pp; French.
XX	
CC	The human monoclonal antibody D7C2, of isotype IgM, recognises a
CC	30-32 kD polypeptide on the membrane of rhesus positive red blood
CC	cells. The antibody agglutinates rhesus positive cells but not
CC	rhesus negative cells and is useful diagnostically and also for
CC	preventing haemolysis in new-born rhesus positive babies.
CC	Recombinant IgM-D7C2 can be produced by insect cells which have
CC	been transformed by a baculoviral vector comprising a D7C2
CC	expression cassette. The present sequence encodes a recombinant
CC	IgM-D7C2 heavy chain fused to a mouse VH signal peptide.
XX	
SQ	Sequence 1418 BP; 333 A; 458 C; 378 G; 249 T; 0 other;
	Query Match 85.4%; Score 1221.6; DB 17; Length 1418;
	Best Local Similarity 92.9%; Pred. No. 7e-235;
	Matches 1317; Conservative 0; Mismatches 89; Indels 12; Gaps 3
QY	13 TGGTTCTTCCTCTCTGTGTGCAGACTCCCAGATGGGTCCTGCCAGTGAAAGTCSAG 72
Db	13 TGTATCATCTCTCTTGTGTGAACAACAGCTACAGGTGTCCACTCCAGGTCCAACTGCAG 72
QY	73 CAGTGGGGCGAAGGACTTCTCAGCCCTTCGGAGACCCTGTCCCGACCTGGGTGTCTCT 132
Db	73 CAGTGGGGCGCAGGACTGTGTGAAGCCTTCGGAGACCCTGTCCCTCACCTGACTGTCTAT 132
QY	133 GTGGGCTCCATCAGCGGTGTACTACTCTGGACCTGGATCCGCCAGACCCACAGGGAGGGGA 192
Db	133 GTGGGTCCTTCAGTGGT---TACTACTGGAGCTGGATCCGCCAGCCCCAGGAGAGGG 189
QY	193 CTGGAGTGGATTGGCCATATTATGGTAATGGTGGACCAACCAACTCAATCCCTCCCTC 252
Db	190 CTGGAGTGGATTGGGGAAATCAA---TCATAGTGGAGCACCAACTCAACCCGTCCCTC 246
QY	253 AAGAGTCGAGTCACCATTTCAAAGACACAGCTCCAAGAACAGATTCTTCCTGAACTTGAAT 312
Db	247 AAGAGTCGAGTCACCATATCAGTAGACACGCTCCAAGAACAGATTCTTCCTGAAACTGAAC 306
QY	313 TCTGTGACCGACGCGACACGSCCTCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGC 372
Db	307 TCTGTGACCGCGCGAACAGGCTGTATTACTGTGCGAGGG-----CCCAGAGTAT 360
QY	373 ACAACCATTTGTTATGGCGGCTGGGTGCATGTCTGGGGCCCGGAGACCTGGTCACCGTC 432
Db	361 AAATGGAAGTATCATGGGACTGGTTTCGACCCCTGGGGCCAAGTACCACTGTACCGTC 420
QY	433 TCCTCAGCTAGACACCAAGGGCCCATTCGGTCTTCCCCCTTGGCACCCCTCTCCAAAGACCC 492
Db	421 TCCTCAGCCCTCCACCAAGGGCCCATTCGGTCTTCCCGCTTGGCACCCCTCTCCAAAGACCC 480
QY	493 TCTGGGGGCACACGGGCCCTGGGCTGCTGTGAAGGACTACTTCCCGGAACCGGTGAGC 552
Db	481 TCTGGGGGCACACGGGCCCTGGGCTGCTGTGAAGGACTACTTCCCGGAACCGGTGAGC 540
QY	553 GTGTCTGTGGAATCTCAGGGGCCCTGTACACAGCGGCGTGACACACTTTCCTCCGGCTGTCTTACAG 612
Db	541 GTGTCTGTGGAATCTCAGGGGCCCTGTACACAGCGGCGTGACACACTTTCCTCCGGCTGTCTTACAG 600
QY	613 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGCCCTCCACAGACTTTGGGACCC 672
Db	601 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGAACCGTGCCCTCCACAGACTTTGGGACCC 660

QY	673	CAGACCTCAATCTCGAACGCGAATCA	CAAGCCCAAGCAACCAAGGTGGACAAGAAAGCA	733
Db	661	CAGACCTCAATCTCGAACGCGAATCA	CAAGCCCAAGCAACCAAGGTGGACAAGAAAGCA	720
QY	733	GAGCCCAAAATCTTGTCGACAAACCT	CACATGCCCCCGTCCGACCACTGAACTCCTG	792
Db	721	GAGCCCAAAATCTTGTCGACAAACCT	CACATGCCCCCGTCCGACCACTGAACTCCTG	780
QY	793	GGGGGACCGTCAGCTTCTCTCTCTCT	CCCCCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGG	852
Db	781	GGGGGACCGTCAGCTTCTCTCTCTCT	CCCCCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGG	840
QY	853	ACCCTTGAGGTACATCGGTGGTGGAG	CGTGAGCCACAAGACCCCTGAGGTCAAGTTC	912
Db	841	ACCCTTGAGGTACATCGGTGGTGGAG	CGTGAGCCACAAGACCCCTGAGGTCAAGTTC	900
QY	913	AACGTGTACGTGGAGCGGCGTGGAGG	TGCATAATGCCAAGACAAGCCGCGGAGGAGCAG	972
Db	901	AACGTGTACGTGGAGCGGCGTGGAGG	TGCATAATGCCAAGACAAGCCGCGGAGGAGCAG	960
QY	973	TACAACGACGCTACCGGTGGTGGTGG	TGCGTCTTCAACGACCAAGGACTGGCTGAAT	1032
Db	961	TACAACGACGCTACCGGTGGTGGTGG	TGCGTCTTCAACGACCAAGGACTGGCTGAAT	1020
QY	1033	GGCAAGGAGTACAAGTGCAGAGGTCTC	CAACAAAGCCCTCCAGCCCTCATCGAGAAACCC	1092
Db	1021	GGCAAGGAGTACAAGTGCAGAGGTCTC	CAACAAAGCCCTCCAGCCCTCATCGAGAAACCC	1080
QY	1093	ATCTCCAAAGCCAAAGGCGACCCGAG	AGCAACACAGGTGTACACCTGCCCCCATCCCGG	1152
Db	1081	ATCTCCAAAGCCAAAGGCGACCCGAG	AGCAACACAGGTGTACACCTGCCCCCATCCCGG	1140
QY	1153	GATGAGCTGACCAAGAACCAAGCTCAG	CGCTTCAAGGCTTCTATCCGAGC	1212
Db	1141	GATGAGCTGACCAAGAACCAAGCTCAG	CGCTTCAAGGCTTCTATCCGAGC	1200
QY	1213	GACATCCCGCTGGAGTGGGAGCAATG	GCGACCGGAGAACCACTACAAGACCAAGCCT	1272
Db	1201	GACATCCCGCTGGAGTGGGAGCAATG	GCGACCGGAGAACCACTACAAGACCAAGCCT	1260
QY	1273	CCCGTGTCTGACTCCGACGCGCTCTCT	CTTCTCTTACAGCAAGCTCACCGTGGACAAGAGC	1332
Db	1261	CCCGTGTCTGACTCCGACGCGCTCTCT	CTTCTCTTACAGCAAGCTCACCGTGGACAAGAGC	1320
QY	1333	AGGTGGCAGCAGGGGAACGCTTCTCAT	GCTCCGCTGATGCATGAGGCTTGCAACACCAC	1392
Db	1321	AGGTGGCAGCAGGGGAACGCTTCTCAT	GCTCCGCTGATGCATGAGGCTTGCAACACCAC	1380
QY	1393	TACACGAGAGAGCCCTTCCCTGTCTC	CGGGTAAATG 1430	
Db	1381	TACACGAGAGAGCCCTTCCCTGTCTC	CGGGTAAATG 1418	
RESULT 11				
AAT62868				
ID	AAT62868 standard; DNA; 1404 BP.			
XX	AC AAT62868;			
XX	18-OCT-1997 (first entry)			
DT	Human gamma-4 heavy chain DNA.			
DE				
XX				
KW	CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;			
KW	cynomolgus monkey; autoimmune disease; rheumatoid arthritis;			
KW	leukaemia; lymphoma; graft-versus-host disease; asthma;			
KW	transplant rejection; HIV; therapy; CE9 gamma 4; ss.			
XX				
OS	Homo sapiens.			
XX				
FN	W09709351-A1.			
XX				

KW	CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV; therapy; CE9 gamma-4PE; gs.
OS	Homo sapiens.
XX	
XX	WO9709351-A1.
XX	
XX	13-MAR-1997.
XX	
XX	05-SEP-1996; 96WO-US14324.
XX	
XX	06-SEP-1995; 95US-0523894.
XX	
XX	(IDEC-) IDEC PHARM CORP.
XX	
XX	Hanna N, Newman RA, Reff ME;
PI	
DR	WPI; 1997-201913/18.
DR	P-PSDB; AAW14927.
XX	
PT	Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, esp. useful for treatment of autoimmune disease, e.g. rheumatoid arthritis
PT	
XX	
XX	Disclosure; Page 91-93; 155pp; English.
PS	
XX	
CC	DNA sequences (AAW62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IgG4 Fc binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
CC	
XX	
SQ	Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;
Query Match 81.6%; Score 1168.2; DB 18; Length 1404;	
Best Local Similarity 89.9%; Pred. No. 3.2e-224;	
Matches 1286; Conservative 0; Mismatches 118; Indels 27; Gaps 2	
Qy	1 ATGAAACACGTGGTTCTTCTCTCTCTGGTGGCAGCTCCAGATGGTCTGTCCAG 60
Db	1 ATGAAACACGTGGTTCTTCTCTCTCTGGTGGCAGCCCCAGATGGGTCTGTCCAG 60
Qy	61 GTCAAGCTGCAGCAGTGGGGCGAAGCACTCTTCGAGCCCTCGGAGACCTGTCCCGCACC 120
Db	61 GTCACCTGCAGAGTGGGGCCAGCACTGGTGAAGCCCTCGGAGACCTGTCCCTACC 120
Qy	121 TGGCTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTATCGACCTGGATCCGCCAGACC 180
Db	121 TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC 180
Qy	181 CCAGGAGGGGACTGGAGTGGATTGGCCATATTTATGTAATGTGCGACCAACAATAC 240
Db	181 CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGCAACAATTAC 240
Qy	241 AATCCCTCCCTCAAGAGTCCAGTCAACCATTTTCAAAGACAGCTCCAAGAACCAAGTTCTTC 300
Db	241 AATCCCTCCCTCAACATCGAGTCTCCATTTTCATAGACAGTCCAGAACCTTCTTC 300
Qy	301 CTGAACTTGAAATCTGTGACCGACCGGACACGGCCGCTATTATTACTGTGCGAGAGCCCT 360
Db	301 CTGAAACTGAGGCTCTGACCGCCGCGACACGGCCGCTATTATTACTGTGCGA----- 352

181	CCAGGGAAGGGA	CTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGACCAATTAC	241
241	AATCCCTCCCTC	ACAGAGTCGAGTCACCATTTTCAAAAGACACGTCCTCAAGAAACGAGTTCCTC	300
241	AATCCCTCCCTC	CAACAATCGAGTCTCCATTTCAATAGACAGTCCAAGAACCTCTTCTCC	300
301	CTGAACCTGAAT	TCTGTGACCGACCGGACACGCGCGTCTATTACTGTGCGAGAGCCCT	360
301	CTGAACCTGAGG	TCTGTGACCGCGCGGACACGCGCGTCTATTACTGTGCGA-----	352
361	CGCCCTGATTGC	ACAAACCATTTGTATGCGCGCTGGGTGCGATGTCTGGGGCCGGGAGAC	420
353	-----GTAATA	TATATTGAAATATCTTCACCTGGTTATTATATACTGGGGCCAGGAGTC	402
421	CTGGTCACGCTC	CTCCTCAGCTAGCACAAAGGCGCCATCGGTCTTCCCGCTGSCACCCCTCC	480
403	CTGGTCACGCTC	CTCCTCAGCTAGCACAAAGGCGCATCCGTCTTCCCGCTGGCGCCCTGC	462
481	TCCAAGAGCACCT	CTGGGGGCACAGCGCCCTTGGGCTGCTCGGTCAAGGACTACTTCCCC	540
463	TCCAAGAGCACCT	CCGAGAGCACAGCGCCCTTGGGCTGCTCGGTCAAGGACTACTTCCCC	522
541	GAACCGGTGAG	CGGTGTGCTGAGAACTCAGGCGCCCTGACACAGCGGGTGCACCTTCCGG	600
523	GAACCGGTGAG	CGGTGTGCTGAGAACTCAGGCGCCCTGACACAGCGGGTGCACACCTTCCGG	582
601	GCTGTCTCAGT	CTCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCACG	660
583	GCTGTCTCAGT	CTCCTCAGGACTCTACTCCCTCAGCAGCGGTGTGACCGTGCCTCCACG	642
661	AGCTTGGGACCC	ACAGACTCATCTCTGCAACCGTGAATCACAAAGCCAGCAACACCAAGGTG	720
643	AGCTTGGGACCA	AGACTCATCTGCAACCGTGAATCACAAAGCCAGCAACACCAAGGTG	702
721	GACAAAGAGAG	CGTGTGACAAAACCTGATGCAAAAACCTGATGCAAAAACCTGATGCAAAA	780
703	GACAAAGAGAG	TTGAGTCCAAAATATG-----TCCCCCATGCCCCATGCCCCCAGCA	753
781	CCTGAACTCTG	GGGGGACCGTCACTCTTCTCTTCCCCCAAAACCAAGGACACCTC	840
754	CCTGAGTTCGA	GGGGGACCAATCAGTCTTCTGTCTCCCCCAAAACCAAGGACACTCTC	813
841	ATGATCTCCCG	ACCCCTGAGGTCCATGCGTGGTGGTGGACGTGAGCAGCAAGACCCCT	900
814	ATGATCTCCCG	ACCCCTGAGGTCCATGCGTGGTGGTGGACGTGAGCAGCAAGACCCCT	873
901	GAGGTCAAGTT	CAACTGGTGTGAGCGCGGTGAGGTGCATAATGCCAAGCAAAAGCGG	960
874	GAGGTCAAGTT	CAACTGGTGTGAGCGCGGTGAGGTGCATAATGCCAAGCAAAAGCGG	933
961	CGGGAGAGCAG	GTACAACAGCACTACCGTGTGTGTCAGCGTCTCACCGTCTGACACAG	1020
934	CGGGAGAGCAG	GTACAACAGCACTACCGTGTGTGTCAGCGTCTCACCGTCTGACACAG	993
1021	GACTGGCTGAAT	GGCAAGGAGTCAAGTGCAGGTCTCCAAAGACCGCTCCCGACCCCTC	1080
994	GACTGGCTGAAG	CGCAGAGTACAGTGCAGGTCTCCAAAGACCGCTCCCGTCTCTCC	1050
1081	ATCGAGAAAA	ACCAATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCAAGGTGTACACCTG	1140
1054	ATCGAGAAAA	ACCAATCTCCAAAGCCAAAGGGCAGCCCCCGAGAACCAAGGTGTACACCTG	1110
1141	CCCCCATCCCG	GNATGAGCTGACCAAGAACCAAGTGCAGCTGACCTGCTGGTCAAGGC	1200
1114	CCCCCATCCCG	GNATGAGCTGACCAAGAACCAAGTGCAGCTGACCTGCTGGTCAAGGC	1170
1201	TTCTATCCAG	CGCATCGCCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACCAACTAC	1260
1174	TTCTATCCAG	CGCATCGCCGTGGAGTGGGAGAGCAATGGGACGCGGAGAACCAACTAC	1230
1261	AAGACCAAGC	CTCCGCTGGACTCCGACGGCTCTCTTCTCTATACAGCAAGCTCAC	1320
1234	AAGACCAAGC	CTCCGCTGGACTCCGACGGCTCTCTTCTCTATACAGCAAGCTCAC	1290

QY 1141 CCCCATCCCGGATGAGCTGACCAAGACACAGGTCAGCTGACCTGCTGCTCAAGGC 1200
| | | | |
Db 1138 CCCCATCCCGGATGAGCTGACCAAGACACAGGTCAGCTGACCTGCTGCTCAAGGC 1197
| | | | |
QY 1201 TTCTATCCAGGACATCCCGTGGAGTGAGGAGCAATGGGAGCCGAGAGCAACTAC 1260
| | | | |
Db 1198 TTCTATCCAGGACATCCCGTGGAGTGAGGAGCAATGGGAGCCGAGAGCAACTAC 1257
| | | | |
QY 1261 AAGACACGCTCCCGTGTGACTCCGAGCTCCGAGCTCTTCTTCTTACAGCAAGCTCAC 1320
| | | | |
Db 1258 AAGACACGCTCCCGTGTGACTCCGAGCTCCGAGCTCTTCTTCTTACAGCAAGCTCAC 1317
| | | | |
QY 1321 GTGGACAGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1380
| | | | |
Db 1318 GTGGACAGAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1377
| | | | |
QY 1381 GTGCAACCACTACACGAGAGAGGCTCTCCCTGTCTCCGGTAAATGA 1431
| | | | |
Db 1378 GTGCAACCACTACACGAGAGAGGCTCTCCCTGTCTCCGGTAAATGA 1428
| | | | |

RESULT 15

AAT61241
ID AAT61241 standard; DNA; 1428 BP.
XX AAT61241;
AC AAT61241;
XX
DT 13-MAY-1997 (first entry)
XX
XX Human anti-RSV monoclonal antibody RF-1 heavy chain DNA.
XX
XX Monoclonal antibody; MAb; RF-1; RF-2; respiratory syncytial virus;
KW RSV; fusion protein; F-protein; vaccine; immunotherapy; therapy;
KW Epstein Barr virus; immortalisation; recombinant antibody; ss.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT sig_peptide 1..57
FT /*tag= a
FT mat_peptide 58..1425
FT /*tag= b
XX
XX WO9640252-A1.
XX
XX 19-DEC-1996.
XX
XX 06-JUN-1996; 96WO-US10070.
XX
XX 07-JUN-1995; 95US-0488376.
XX
XX (IDEC-) IDEC PHARM CORP.
XX
XX Brans P, Charnat SS, Heard CJ, Newman RA, Pan L;
PI Walsh EE;
XX
XX WPI; 1997-099892/09.
DR P-PSDB; AAW11639.
XX
XX Human monoclonal antibody specific for respiratory syncytial virus
PT fusion protein - used for the prevention and treatment of RSV
PT infection
XX
XX Claim 9; Fig 9b-c; 85pp; English.
XX
XX A DNA sequence (AAT61241) codes for a polypeptide (AAW11639) comprising
CC a leader sequence, RF1 heavy chain variable region (see also
CC AAW11637), and human gamma 1/constant region. RF1 is a human
CC monoclonal antibody (hMAb) specific for the fusion protein of
CC respiratory syncytial virus (RSV). The DNA sequence, in vector
CC NEOSPLA, can be used to produce the light chain construct in
CC transfected eukaryotic (e.g. CHO) cells. RF-1 and RF-2 heavy
CC and light chain constructs (see also AAT61240, AAT61242, AAT61279) are

CC similarly used. The transfected host cells provide a constant,
CC stable supply of anti-RSV F-protein hMABs for use in the treatment
CC or prevention of RSV infection.
XX
SQ Sequence 1428 BP; 326 A; 465 C; 372 G; 265 T; 0 other;
Query Match 78.6%; Score 1125.2; DB 18; Length 1428;
Best Local Similarity 88.6%; Pred. No. 1.2e-215;
Matches 1256; Conservative 0; Mismatches 153; Indels 9; Gaps 3;
QY 17 TCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTCTCCAGGTGAAGCTGCAGCAGT 76
| | | | |
Db 17 TCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTCTCCAGGTGAAGCTGCAGCAGT 76
| | | | |
QY 77 GGGGGAAGAGCTTCTGCAGCCTTCGGAGACCTGTCCGGACACCTGCTTCTTGTG 136
| | | | |
Db 77 CTGGTCTCTGTGTGTAAGCCACAGAGACCTCAGCTGACCTGCACCTCTCTGGT 136
| | | | |
QY 137 GCTC---CATCAGCGGTCTACTACTGACCTGTGATCCGACAGACCCAGGAGGGAC 193
| | | | |
Db 137 TCTACTCAGCAACCTTAGAATGGGTGTGATCCGTGACCCCTCCGGAAGGCC 196
| | | | |
QY 194 TGGAGTGAATGGCCATATTTATGTAATGTGCGACCACTACAACTACCTCCCTCA 253
| | | | |
Db 197 TAGAATGCTTGGAAACATTTTTCGAGTGACGAGATC---CTTCAGTCTCTCTGA 253
| | | | |
QY 254 AGATCGAGTCAACATTTCAAAGACACGTCAAGAAACAGTTCTTCTGAATTTGAATT 313
| | | | |
Db 254 AGAGCAGACTCACACCTCCAGGACACCTCCAGAAAGCAGGTGCTTCAAGCTTGACCA 313
| | | | |
QY 314 CTGTGACGCGCGACACGCGCTCTATTACTGTGCGAGAGGCCCTCGCCCTGATTGA 373
| | | | |
Db 314 ACGTGGACCTGTGGACACAGCCATATTAATCTGTGC---ACGGGTAGACTGTATGACA 370
| | | | |
QY 374 CAACATTTGTTATGGCGCTGGTTCGATGCTTGGGCGCCGGGAGACCTGTGCACGCTCT 433
| | | | |
Db 371 TCAATGCTTATTAACCTATACTACCTGGATATTGGGGGAGGAACTTGTTCACCGTCT 430
| | | | |
QY 434 CTTAGCTAGCAACAAAGGCGCATCGTCTTCCCTTGGCAGCCCTCTCTCCAAAGACCT 493
| | | | |
Db 431 CTTAGCTAGCAACAAAGGCGCATCGTCTTCCCTTGGCAGCCCTCTCTCCAAAGACCT 490
| | | | |
QY 494 CTGGGGGACACGCGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 553
| | | | |
Db 491 CTGGGGGACACGCGCGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
| | | | |
QY 554 TGTCTGTGAACCTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGGCTGTCTTACAGT 613
| | | | |
Db 551 TGTCTGTGAACCTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGGCTGTCTTACAGT 610
| | | | |
QY 614 CTTAGGACTCTACTCTCTCAGCAGCGTGTGACCGTCTCCAGCAGCTTGGGACCC 673
| | | | |
Db 611 CTTAGGACTCTACTCTCTCAGCAGCGTGTGACCGTCTCCAGCAGCTTGGGACCC 670
| | | | |
QY 674 AGACCTATCATCTGCAACCTGTAATCAAGCCCGAGCAACACCAAGGTGGACAGAAAGCAG 733
| | | | |
Db 671 AGACCTATCATCTGCAACCTGTAATCAAGCCCGAGCAACACCAAGGTGGACAGAAAGCAG 730
| | | | |
QY 734 AGCCCAAAATCTTGTGACAAAACCTCACATATGCCACCGTGGCGAGCAGCTGAACTCTCTGG 793
| | | | |
Db 731 AGCCCAAAATCTTGTGACAAAACCTCACATATGCCACCGTGGCGAGCAGCTGAACTCTCTGG 790
| | | | |
QY 794 GGGGACCGTCACTCTTCTTCTTCCCAAAACCAAGGACACCTCTCATGATCTCCCGGA 853
| | | | |
Db 791 GGGGACCGTCACTCTTCTTCTTCCCAAAACCAAGGACACCTCTCATGATCTCCCGGA 850
| | | | |
QY 854 CCCCCTGAGGTCACTGCGTGTGTGGAGTGAGGACCAAGAGACCTCTGAGGTCAAGTTCA 913
| | | | |
Db 851 CCCCCTGAGGTCACTGCGTGTGTGGAGTGAGGACCAAGAGACCTCTGAGGTCAAGTTCA 910
| | | | |
QY 914 ACTGCTAGCTGGACCGCTGGAGGTGCATATATCAAGACAAAGCCCGGGAGGAGCAGT 973
| | | | |
Db 911 ACTGCTAGCTGGACCGCTGGAGGTGCATATATATCAAGACAAAGCCCGGGAGGAGCAGT 970
| | | | |

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 17:51:01 ; Search time 188.659 Seconds
(without alignments)
10227.493 Million cell updates/sec

Title: US-09-576-424-3

Perfect score: 1431

Sequence: 1 atgaaacacctgtgtgtttt.....ccctgtctccgggtaaatga 1431

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	9	US-10-124-905-3
2	1431	100.0	1431	9	US-09-948-429B-3
3	1429.4	99.9	1431	9	US-10-073-138-2
4	1315.8	91.9	1431	9	US-10-124-905-11
5	1315.8	91.9	1431	9	US-09-948-429B-11
6	1314.2	91.8	1431	9	US-10-073-138-6
7	1171.4	81.9	1404	9	US-10-211-357-7
8	1168.2	81.6	1404	9	US-10-211-357-11
9	1166.6	81.5	1404	9	US-10-211-357-9
10	1123.6	78.5	1428	10	US-09-740-002-17
11	1117.2	78.1	1437	9	US-10-124-905-7
12	1117.2	78.1	1437	9	US-09-948-429B-7
13	1117.2	77.8	1437	9	US-10-073-138-4
14	1113.4	77.8	1798	10	US-09-925-299-230
15	1113.4	77.8	1798	10	US-09-925-299-230
16	1112.4	77.7	1428	10	US-09-740-002-19
17	1102	77.0	1599	10	US-09-954-456-789
18	1102	77.0	1599	10	US-09-954-456-789
19	1100.8	76.9	1427	12	US-10-066-895-20

Result No.	Score	Query Match	Length	ID	Description
20	1100.8	76.9	1427	12	US-10-066-895-25
21	1098.8	76.8	1449	10	US-09-747-669-1
22	1098.8	76.8	1449	10	US-09-747-669-2
23	1097.6	76.7	1427	12	US-10-066-895-27
24	1092.8	76.4	6284	12	US-10-066-895-14
25	1092.2	76.3	1617	10	US-09-822-830A-571
26	1090.6	76.2	8120	9	US-09-726-258-68
27	1089.2	76.1	1356	10	US-09-822-898A-27
28	1088.8	76.1	1539	10	US-09-822-849A-87
29	1087.6	76.0	1615	10	US-09-822-849A-111
30	1087	76.0	9199	9	US-09-911-692-3
31	1087	76.0	9209	9	US-09-911-703-3
32	1087	76.0	9209	9	US-09-905-928-2
33	1087	76.0	9209	9	US-10-096-984-2
34	1087	76.0	18986	9	US-10-109-853-2
35	1086.8	75.9	1598	10	US-09-822-849A-103
36	1086	75.9	1605	10	US-09-822-830A-501
37	1083.8	75.7	9182	9	US-09-927-122-41
38	1083.8	75.7	9182	9	US-09-927-121B-89
39	1081	75.5	1404	10	US-09-825-012-10
40	1081	75.5	3300	9	US-10-020-786-2
41	1078.4	75.4	2196	10	US-09-825-012-44
42	1078.4	75.4	2196	10	US-09-825-012-45
43	1078.4	75.4	2226	10	US-09-825-012-53
44	1078.4	75.4	2226	10	US-09-825-012-54
45	1078	75.3	1347	10	US-09-736-371B-20

ALIGNMENTS

RESULT 1
US-10-124-905-3
; Sequence 3, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10124,905
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs

RESULT 3
US-10-073-138-2
; Sequence 2, Application US/10073138
; Publication No. US20020187146A1
; " GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE H
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0.
; Version #1.30

Db 1054 ATCGAGAAACCATCTCAAAGCCAAAGGCGAGCCCGGAGACCCACAGGTGTACACCCGTG 1113
Qy 1141 CCCCATCCCGGAGTGAAGTGAACCAAGAGCCAGGTGAGCTGAGCTGTGTCAAAGGC 1200
Db 1114 CCCCATCCCGGAGGAGATGACCAAGAACCAAGGTGAGCTGAGCTGTGTCAAAGGC 1173
Qy 1201 TTCTATCCCGAGGACATGCGCTGGAGTGGGAGAGCAATGGGACCGGAGAACCACTAC 1260
Db 1174 TTCTATCCCGAGGACATGCGCTGGAGTGGGAGAGCAATGGGACCGGAGAACCACTAC 1233
Qy 1261 AAGACCAAGCCTCCCGTGTGAGTCTCCGAGCGGCTCTCTTCTCTTACAGCAAGCTCAC 1320
Db 1234 AAGACCAAGCCTCCCGTGTGAGTCTCCGAGCGGCTCTCTTCTCTTACAGCAAGCTCAC 1293
Qy 1321 GTGGACAGAGCAGGTGGGAGCAGGGAACGTCTTCTCATGCTCCGATGATGATGAGGT 1380
Db 1294 GTGGACAGAGCAGGTGGGAGGAGGAATGTCTTCTCATGCTCCGATGATGATGAGGT 1353
Qy 1381 GTGCACACCACTACACGAGAGAGCCTCTCCCTGTCTCCGGTAAATGA 1431
Db 1354 GTGCACACCACTACACAGAGAGCCTCTCCCTGTCTCTGGGTAAATGA 1404

RESULT 8

US-10-211-357-11

; Sequence 11, Application US/10211357

; Publication No. US2003007725A1

; GENERAL INFORMATION:

; APPLICANT: Hanna, Nabil

; Newman, Roland A.

; Reff, Mitchell E.

; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

; Therapy

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314-3187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/211,357

; FILING DATE: 05-Aug-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/612,914A

; FILING DATE: 10-Jul-2000

; APPLICATION NUMBER: US 08/523,894

; FILING DATE: 06-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teekin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1404 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; POSITION IN GENOME:

; CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E

; mutation

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1404

; FEATURE:

; NAME/KEY: mat peptide

; LOCATION: 1..1404

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-10-211-357-11

Query Match 81.6%; Score 1168.2; DB 9; Length 1404;
Best Local Similarity 89.9%; Pred No. 3.7e-313;
Matches 1286; Conservative 0; Mismatches 119; Indels 27; Gaps 2;
Qy 1 ATGAAACACCTGTGGTCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTGCCAG 60
Db 1 ATGAAACACCTGTGGTCTTCTCTCTCTGTGGCAGCTCCAGATGGGTCTGTGCCAG 60
Qy 61 GTGAAGCTGACAGCTGGGGGGAAGGACTTCTGCAGCCTTCGGAGACCTGTCCCGCACC 120
Db 61 GTGCAGCTGACAGGAGTCGGGGCCAGGACTGGTGAAGCCTTCGGAGACCTGTCCCGCACC 120
Qy 121 TGGCTTGTCTCTGTGGCTCCATCAGCGGTTACTACTCTGACCTGATCCGCCAGACC 180
Db 121 TGCAGTGTCTGTGGTCTCCATCAGCGGTGACTATTATTGGTCTGGATCGCCAGTCC 180
Qy 181 CCAGGGAGGGACTGGAGTGGCAATTTATGGTAAATGGTGCACCACTTTC 240
Db 181 CCAGGAGGAGCTGGAGTGGCTACATCTATGSCAGTGGTGGGGGACCAATTC 240
Qy 241 AATCCCTCCCTCAAGAGTCGAGTCAACATTTCAAAGACACGTCGAGAACGAGTTC 300
Db 241 AATCCCTCCCTCAACATTCGAGTCTCCATTTCAATAGACAGTCGAGAACCTCTTC 300
Qy 301 CTGAACCTTGAATCTGTGACCGACGCGGACGCGCTCTATTACTGTGCGAGAGGCCCT 360
Db 301 CTGAACCTGAGTCTGTGACCGCGGACGCGGCTCTATTACTGTGCGGACGCGGAC 352
Qy 361 CGCCCTGATTCACAAACCATTTGTTATGGCGGCTGGGTGATGTCGTGGGGCCCGGAGAC 420
Db 353 -----GTAATATATGAAATACTTCACTGGTTATTATCTGGGGCCAGGAGTTC 402
Qy 421 CTGTGACCGTCTCTCAGCTAGCACCAAGGGCCCATGGTCTTCCCTCTGGCACCTTCC 480
Db 403 CTGTGACCGTCTCTCAGCTAGCACCAAGGGCCCATCGTCTTCCCTCTGGCGCCCTGC 462
Qy 481 TCCAGAGACCTCTGGGGGACACGCGCCCTGGGTGCTGCTGCTCAAGGACTACTTCCC 540
Db 463 TCCAGAGACCTCTCGAGAGCACAGCGCCCTGGGTGCTGCTGCTCAAGGACTACTTCCC 522
Qy 541 GAAACCGGTGACCGTGTGTGGAACTCAGGGCCCTTGACAGCGGCTGCACACCTTCCCG 600
Db 523 GAAACCGGTGACCGTGTGTGGAACTCAGGGCCCTTGACAGCGGCTGCACACCTTCCCG 582
Qy 601 GCTGTCTTACAGTCTCTCAGGACTTACTCTCTCAGCAGCGTGGTACCGTCCCTCCAGC 660
Db 583 GCTGTCTTACAGTCTCTCAGGACTTACTCTCTCAGCAGCGTGGTACCGTCCCTCCAGC 642
Qy 661 AGCTTGGGACCCAGACCTACATCGAAGTGAATCAAGAGCCGAGCAACCAAGGTG 720
Db 643 AGCTTGGGACCCAGAGACCTACACCTGCAACGTAGATCAAGAGCCGAGCAACCAAGGTG 702
Qy 721 GACAAGAAAGCAGAGCCCAATCTTGTGACAAAATCTACACATGCCACCTGCCAGCA 780
Db 703 GACAAGAGAGTTGAGTCCAAATATGG-----TCCCCCATGCCCATGCCAGCA 753
Qy 781 CCTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTTC 840
Db 754 CCTGAGTTGAGGGGGGACCATCAGTCTTCTCTTCCCCCAAAACCCCAAGGACACCTTC 813
Qy 841 ATGATCTCCCGGACCCCTCAGGTCAATGCTGTGTGGTGGAGCGTGGAGCAGAACCTTC 900
Db 814 ATGATCTCCCGGACCCCTCAGGTCAATGCTGTGTGGTGGAGCGTGGAGCAGAACCTTC 873

Db 643 ACCTTGGGCGCAAGACCTACACCTGCAACGTAGATCAACAGCCGACGACACCAAGGTG 702
Qy 721 GACAGAAAGACAGAGCCCAAAATCTTGTGACAAATCTACACATGCCCAACCGTGGCCAGCA 780
Db 703 GACAGAGAGTTGAGTCCAAATATG-----TCCCCCATGCCATCATGCCAGCA 753
Qy 781 CTTGAATCTCTGGGGGACCGTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
Db 754 CTTGAGTTCCAGGGGGGACCATCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
Qy 841 ATGATCTCCCGACCCCTCAGGTACATCGTGGTGGTGGAGCTGAGCCACCAAGACCTC 900
Db 814 ATGATCTCCCGACCCCTCAGGTACATCGTGGTGGTGGAGCTGAGCCACCAAGACCTC 873
Qy 901 GAGGTCAAGTTCAACTGTTACCTGACGCGCTGGAGGTGCATAATGCCCAAGCAAAAGCG 960
Db 874 GAGGTCCAGTTCAACTGTTACCTGATGCGGTGGAGGTGCATAATGCCCAAGCAAAAGCG 933
Qy 961 CCGGAGGACAGTACACAGCAGTACCGTGTGGTGGAGCTCTACCGTCTCTGACACG 1020
Db 934 CCGGAGGACAGTACACAGCAGTACCGTGTGGTGGAGCTCTACCGTCTCTGACACG 993
Qy 1021 GACTGCTCAATGGCAAGGAGTACAGTCAAGGTCTCCAAAGGCTCTCCAAAGGCTCTCCAGCC 1080
Db 994 GACTGCTCAATGGCAAGGAGTACAGTCAAGGTCTCCAAAGGCTCTCCAAAGGCTCTCCAGCC 1053
Qy 1081 ATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCCCTG 1140
Db 1054 ATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCAAGGTGTACACCCCTG 1113
Qy 1141 CCCCACATCCCGGATGAGCTGACCAAGAACGAGGTGAGCTGACCTGACCTGCTCAAGGC 1200
Db 1114 CCCCACATCCCGGAGAGATGACCAAGAACGAGGTGAGCTGACCTGACCTGCTCAAGGC 1173
Qy 1201 TTCTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGCAGCGGAGAACCAACTAC 1260
Db 1174 TTCTATCCAGCAGCATCCCGTGGAGTGGAGAGCAATGGCAGCGGAGAACCAACTAC 1233
Qy 1261 AAGACACACCTCCCGTGTGGACTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1234 AAGACACACCTCCCGTGTGGACTCCGACGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293
Qy 1321 GTGACAAAGCAGAGTGGCAGAGGGGAACGCTTCTATGCTCCGTGTATGATGAGGT 1380
Db 1294 GTGACAAAGCAGAGTGGCAGAGGGGAATGCTTCTCATGCTCCGTGTATGATGAGGT 1353
Qy 1381 CTGCAACCACTACACGAGAGAGCTCTCCCTGCTCTCCGGTAAATGA 1431
Db 1354 CTGCAACCACTACACAGAGAGCTCTCCCTGCTCTCCGGTAAATGA 1404

RESULT 10

US-09-740-002-17
; Sequence 17, Application US/09740002
; Patent No. US20020001798A1
; GENERAL INFORMATION:
; APPLICANT: BRAMS, PETER
; APPLICANT: MORROW, PHILLIP
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
; TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
; FILE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
; FILE REFERENCE: 037003-0275759
; CURRENT APPLICATION NUMBER: US/09/740,002
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/335,697
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 08/488,376
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 1428

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1425)
US-09-740-002-17
Query Match 78.5%; Score 1123.6; DB 10; Length 1428;
Best Local Similarity 88.5%; Pred. No. 7.9e-301;
Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;
Qy 17 TCTTCT 76
Db 17 TCTTCT 76
Qy 77 GGGCGAAGGACTTCTGACGCTTTCGGAGACCTCTGCGACCTCTGCGACCTCTGCGTGTCTCTG 136
Db 77 TGTGCT 136
Qy 137 GCTC---CATCAGCGGTTTACTACTTACTTACTTACTTACTTACTTACTTACTTACTTACTTACT 193
Db 137 TCTCACTCAGCAACCTTAGAATGGGTGTGACCTCGTACGCCCCCGGGAAGGCC 196
Qy 194 TGGAGTGAATGGCCATATTTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGTATGT 253
Db 197 TAGAATGGCTTGGAAACATTTTTCGAGTGTAGAGAGTCT---CTTCAGTCTCTCTCTCTCT 253
Qy 254 AGAGTCGAGTCAACATTTTCAAAAGACAGCTCCAAAGAACAGTCTTCTCTGAACTTTGAAAT 313
Db 254 AGAGCAGACTCACCACTCTCCAGGACACCTCCAGAAAGCCAGGTGTCTTAAGTTTGACCA 313
Qy 314 CTGTGACGACGCGGACACGCGCTCTATTACTGTGTGAGAGGCTCTGCGCTCTGATTGCA 373
Db 314 ACGTGGACCTCTGTGACACAGCCACATATTACTGTGC---ACGGGTAGGACTGTATGACA 370
Qy 374 CAACCATTTGTTATGCGGCTGGGTCTGATGTCTGGGCGCGGAGACCTGTGACCGTCT 433
Db 371 TCAATGCTTATTAACCTATCTACTTGGATTTATTTGGGCGAGGGAACCTTGGTACCGTCT 430
Qy 434 CCTCAGCTAGCACCAAGGCGCCATCGGTCTTCTCCCTCTGGCACCTCTCTCAAGAGCACCT 493
Db 431 CCTCAGCTAGCACCAAGGCGCCATCGGTCTTCTCCCTCTGGCACCTCTCTCAAGAGCACCT 490
Qy 494 CTGGGGGACACAGCGGCGCTCTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 553
Db 491 CTGGGGGACACAGCGGCGCTCTGGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 550
Qy 554 TGTCTGTGAACTCAGCGCGCTCTGACGCGGCTGACACCTTCCCGGCTGTCTTACAGT 613
Db 551 TGTCTGTGAACTCAGCGCGCTCTGACGCGGCTGACACCTTCCCGGCTGTCTTACAGT 610
Qy 614 CCTCAGGACTCTACTCTCTCTCAGCAGCTGTGTGACCGTCTCTCTCTCAGCAGCTTGGGCA 673
Db 611 CCTCAGGACTCTACTCTCTCTCAGCAGCTGTGTGACCGTCTCTCTCTCAGCAGCTTGGGCA 670
Qy 674 AGACCTACATCTGCAACCGTGAATCAAGCCGACCAACCAAGGTGGGAAGAAGCAG 733
Db 671 AGACCTACATCTGCAACCGTGAATCAAGCCGACCAACCAAGGTGGGAAGAAGCAG 730
Qy 734 AGCCCAATCTGTGCAAAACTCACATGCGCCACCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
Db 731 AGCCCAATCTGTGCAAAACTCACATGCGCCACCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 790
Qy 794 GGGGACCGTCT 853
Db 791 GGGGACCGTCT 850
Qy 854 CCCCCTGAGGTCAATGCGT 913
Db 851 CCCCCTGAGGTCAATGCGT 910
Qy 914 ACTGTGACGTGGACCGGCTGGAGGTGTGATATGCAAGCAAGCCCGGGAGGAGGT 973
Db 914 ACTGTGACGTGGACCGGCTGGAGGTGTGATATGCAAGCAAGCCCGGGAGGAGGT 973

Qy	668	GCACCCAGACCTACATCTGCAACGTGAATCA	CAAGCCGAGCAACCAAGGTGGACAAGA	727
Db	674	GCACCCAGACCTACATCTGCAACGTGAATCA	CAAGCCGAGCAACCAAGGTGGACAAGA	733
Qy	728	AAGCAGAGCCCCAAATCTTTGTGCAAAACT	TCACACATGCCACCGTGGCCGACACCTGAAC	787
Db	734	AAGCAGAGCCCCAAATCTTTGTGCAAAACT	TCACACATGCCACCGTGGCCGACACCTGAAC	793
Qy	788	TCCTGGGGGGACCGCTCAGTCTTCTCTTT	CCCCCCCCAAAACCCAAGGACACCCCTCATGATCT	847
Db	794	TCCTGGGGGGACCGCTCAGTCTTCTCTTT	CCCCCCCCAAAACCCAAGGACACCCCTCATGATCT	853
Qy	848	CCCGGACCCCTGAGGTGCATCTGCTGTGT	GTGGAGCTGAGCCACGAAGACCCCTGAGGTCA	907
Db	854	CCCGGACCCCTGAGGTGCATCTGCTGTGT	GTGGAGCTGAGCCACGAAGACCCCTGAGGTCA	913
Qy	908	AGTTCAACTGTGCTGAGCGGTGGAGGTGC	ATAATGCCAAGCAAAAGCGCGGGAGG	967
Db	914	AGTTCAACTGTGCTGAGCGGTGGAGGTGC	ATAATGCCAAGCAAAAGCGCGGGAGG	973
Qy	968	AGCAGTACAAACAGCAGCTACCGTGTGGT	CAGCGTCTCACCGTCTCTGCACCAAGGACTGGC	1027
Db	974	AGCAGTACAAACAGCAGCTACCGTGTGGT	CAGCGTCTCTCACCGTCTCTGCACCAAGGACTGGC	1033
Qy	1028	TGAATGGCAAGGATACAAAGTGC	AAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGA	1087
Db	1034	TGAATGGCAAGGATACAAAGTGC	AAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGA	1093
Qy	1088	AAACCATCTCCAAAGCCAAAGGGCAGCC	CGGAGAACCAAGGTGTACACCTGCCCCCAT	1147
Db	1094	AAACCATCTCCAAAGCCAAAGGGCAGCC	CGGAGAACCAAGGTGTACACCTGCCCCCAT	1153
Qy	1148	CCCGGGATGAGTGCACCAAGAACAGGT	CAGCGTCTCACCGTCTCTCAAGGCTTCTATC	1207
Db	1154	CCCGGGATGAGTGCACCAAGAACAGGT	CAGCGTCTCTCACCGTCTCTCAAGGCTTCTATC	1213
Qy	1208	CCAGCGACATCCCGTGGAGTGGGAGAG	CAATGGGACGCCGAGAACAACTACAAGACCA	1267
Db	1214	CCAGCGACATCCCGTGGAGTGGGAGAG	CAATGGGACGCCGAGAACAACTACAAGACCA	1273
Qy	1268	GGCTTCCGCTGCTGAGTCCGACGGCT	CTTCTCTCTACAGCAAGCTCACCGTGGACA	1327
Db	1274	GGCTTCCGCTGCTGAGTCCGACGGCT	CTTCTCTCTACAGCAAGCTCACCGTGGACA	1333
Qy	1328	AGACGAGTGGCAGCAGGGGAACGTCTT	CTCATGCTCGTGCATGCATGAGGCTCTGCACA	1387
Db	1334	AGACGAGTGGCAGCAGGGGAACGTCTT	CTCATGCTCGTGCATGCATGAGGCTCTGCACA	1393
Qy	1388	ACCACTACGACAGAAGCCCTCTCCCT	GTCTCCGGGTAAATGA	1431
Db	1394	ACCACTACGACAGAAGCCCTCTCCCT	GTCTCCGGGTAAATGA	1437

RESULT 13
US-10-073-138-4
; Sequence 4, Application US/10073138
; Publication No. US20020187146A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, Darrell R.
; HANNA, Nabil
; BRAMS, Peter
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
; INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
; AND B7.2 CO-STIMULATORY ANTIGENS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:


```
QY 626 ACTCCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGCCACCCAGACCTACATCT 685
Db 762 ACTCCCTCAGCAGCGTGTGACCGTCCCTCAGCAGCTTGGCCACCCAGACCTACATCT 821
QY 686 GCAACGTGAATCAACAGCCAGCAACCAACAGGTGACAGAAAGCAGAGCCCAATCTT 745
Db 822 GCAACGTGAATCAACAGCCAGCAACCAACAGGTGACAGAAAGCAGAGCCCAATCTT 881
QY 746 GTGACAAAATCAACATGCCACCGTGGCCAGCACCCTGAACCTCTCTGGGGGACCGCTAG 805
Db 882 GTGACAAAATCAACATGCCACCGTGGCCAGCACCCTGAACCTCTCTGGGGGACCGCTAG 941
QY 806 TCTTCTCTCTCCCTCCCAACCAACAGCAGCACCCTCATGATCTCCCGGACCCCTGAGTCA 865
Db 942 TCTTCTCTCTCCCTCCCAACCAACAGCAGCACCCTCATGATCTCCCGGACCCCTGAGTCA 1001
QY 866 CATGCGTGTGTGGAGCTGAGCCAGCAAGACCCCTGAGGTCAAGTTCAACTGTCGTGG 925
Db 1002 CATGCGTGTGTGGAGCTGAGCCAGCAAGCACCCTGAGGTCAAGTTCAACTGTCGTGG 1061
QY 926 ACGGCGTGAAGTGTCAATATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAACAGCAGT 985
Db 1062 ACGGCGTGAAGTGTCAATATGCCAAGCAAAAGCCGCGGAGGAGCAGTACAAACAGCAGT 1121
QY 986 ACGGTGTGTGACGCTCTCCTCAGTCCAGCAAGACCCCTGAGGTCAAGTTCAACTGTCGTGG 1045
Db 1122 ACGGTGTGTGACGCTCTCCTCAGTCCAGCAAGCACCCTGAGGTCAAGTTCAACTGTCGTGG 1181
QY 1046 AGTGCAAGTGTCTCAAAAGCCCTCCAGCCCTCCAGCAAGCAACCATCTCCAAAGCCA 1105
Db 1182 AGTGCAAGTGTCTCAAAAGCCCTCCAGCCCTCCAGCAAGCAACCATCTCCAAAGCCA 1241
QY 1106 AAGGGCAGCCCGAGCAACCAAGGTGTACACCTCTGCCCTCATCCCGGAGTGAAGTGAAC 1165
Db 1242 AAGGGCAGCCCGAGCAACCAAGGTGTACACCTCTGCCCTCATCCCGGAGTGAAGTGAAC 1301
QY 1166 AGAACCGTGTGACGCTGACCTGCTGTGTAAGAGGTCTTATCCAGCGGACATCGCGGTGG 1225
Db 1302 AGAACCGTGTGACGCTGACCTGCTGTGTAAGAGGTCTTATCCAGCGGACATCGCGGTGG 1361
QY 1226 AGTGGAGAGCAATGGGAGCCGAGCAACCACTACAGACCAAGCAGCTCCCGTGTGGACT 1285
Db 1362 AGTGGAGAGCAATGGGAGCCGAGCAACCACTACAGACCAAGCAGCTCCCGTGTGGACT 1421
QY 1286 CCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGCAGGAGGAGGAGGAGG 1345
Db 1422 CCGACGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGCAGGAGGAGGAGGAGG 1481
QY 1346 GGAACGTCTTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGATGATGAT 1405
Db 1482 GGAACGTCTTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGATGATGAT 1541
QY 1406 GCCTCTCCCTGTCTCCGGTAAATGA 1431
Db 1542 GCCTCTCCCTGTCTCCGGTAAATGA 1567
```

RESULT 15

```
US-09-925-299-230
; Sequence 230, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 230
; LENGTH: 1798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (15)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (31)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (501)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (1798)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-230
```

Query Match 77.8%; Score 1113.4; DB 10; Length 1798;

Best Local Similarity 87.6%; Pred. No. 5.5e-298;

Matches 1232; Conservative 8; Mismatches 155; Indels 11; Gaps 2;

```
QY 26 TCCTGGTGGAGCTCCAGATGGTCTCTGCCAGTGAAGCTGAGTGGGGGAG 85
Db 173 TCCTGGTGGTCTTTTAAGAGGTGTCCAGTGTCCAGTGTGGTGGAGTCTGGGGAG 232
QY 86 GACTTCTCAGCCTTCGGAGACCTGTCCCGACCTGGTCTCTCTGGTGGCTCATCA 145
Db 233 GCGTGGTCCAGCTGGGAGGTCCCTGAGACTCTCTCTGTGACGCTCTGGATTCACTTCA 292
QY 146 GCGGTACTACTACTGAGACCTGGATCCCGCAGACCCAGAGGAGGACTGGAGTGGATTG 205
Db 293 ---GTAGCTATGGATGCACTGGGTCCCGCAGGCTCCAGGCAAGGGGTGGAGTGGTGG 349
QY 206 GCCATATTATGTAAAGTGGCGACCACTAACAATCCCTCTCCCTCAAGAGTGGAGTCA 265
Db 350 CAGTATATATATGATGAAAGTAAATAATCTATGACAGACTCCGTGAAGGCCGATTC 409
QY 266 CCATTTCAAAAGACACGTCCTCAAGACCAAGTCTTCTCTGAACTTGAATCTGTGACCGAG 325
Db 410 CCATCTCCAGAGACAAATTCACAGAACACGCTGTATCTGCAAAATGAACAGCCTGAGAGCTG 469
QY 326 CGGACACGCGCTCTATTACTGTGCGAGAGGCGCTCGGCCCTGATTGCAACAACCATTTGTT 385
Db 470 AGGACACGCGCTGTATTACTGTGCGAGAGANGTTACTATGTTCCGAAAGCATCTACTA 529
QY 386 ATGGCGGCTGGGTGATGTCTGGGGCCCGGAGACCTGGTCAACCTCTCTCAGCTAGCA 445
Db 530 CTA-----CTTTGACTCTGGGCGCAGGAAACWCTGGTCAACCTCTCAGCTTCA 581
QY 446 CCAAGGGCCCATCGTCTTCCCTCCGACACCTCTCCAGAGACACCTCTGGGGGACAG 505
Db 582 CCAAGGGCCCATCGTCTTCCCTCCGACACCTCTCCAGAGACACCTCTGGGGGACAG 641
QY 506 CGGCGCTGGGCTGCTGTCAAGGACTACTTCCCGCAACCGGTGACGCTGTGCGGAAC 565
Db 642 CGGCGCTGGGCTGCTGTCAAGGACTACTTCCCGCAACCGGTGACGCTGTGCGGAAC 701
QY 566 CAGCGCGCTGACCAAGCGGTGTCAACCTTCCCGGTGTCTTACAGTCTCAGACTCT 625
Db 702 CAGCGCGCTGACCAAGCGGTGTCAACCTTCCCGGTGTCTTACAGTCTCAGACTCT 761
QY 626 ACTCCCTCAGCAGCGTGTGACGCTGCGCTCCAGCAGCTTGGGACCCAGCTTACATCT 685
Db 762 ACTCCCTCAGCAGCGTGTGACGCTGCGCTCCAGCAGCTTGGGACCCAGCTTACATCT 821
```

QY 686 GCAAGCTGAATCACAAGCCCAAGCCAGACACCAAGGTGGACAGAAAGCAGAGCCCAATCTT 745
Db |||||||:|||||
822 GCAAGCTGAATCACAAGCCCAAGCCAGACACCAAGGTGGACAGAAAGTGTAGCCCAATCTT 881
QY 746 GTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACCTCTGGGGGAGCCGTGAG 805
Db |||||||:|||||
882 GTGACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACCTCTGGGGGAGCCGTGAG 941
QY 806 TCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 865
Db |||||||:|||||
942 TCTTCTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 1001
QY 866 CATGGTGGTGGTGGAGCTGAGCGACGAGAGCCCTGAGGTCAAGTCAACTGCTACGTGG 925
Db |||||||:|||||
1002 CATGGTGGTGGTGGAGCTGAGCGACGAGAGCCCTGAGGTCAAGTCAACTGCTACGTGG 1061
QY 926 ACGGCTGGAGTGTCAATATGCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGT 985
Db |||||||:|||||
1062 ACGGCTGGAGTGTCAATATGCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGT 1121
QY 986 ACCGTGGTTCAGCGTCTCAACCAAGCCCTCCAGCCCCCATCGAGAAACCCTCTCCAAAGCCA 1045
Db |||||||:|||||
1122 ACCGTGGTTCAGCGTCTCAACCAAGCCCTCCAGCCCCCATCGAGAAACCCTCTCCAAAGCCA 1181
QY 1046 AGTGAAGGTCTCCAAACCAAGCCCTCCAGCCCCCATCGAGAAACCCTCTCCAAAGCCA 1105
Db |||||||:|||||
1182 AGTGAAGGTCTCCAAACCAAGCCCTCCAGCCCCCATCGAGAAACCCTCTCCAAAGCCA 1241
QY 1106 AAGGCGAGCCCGAGAACCAACAGGTGTACACCCCTGCCCCATCCCGGGATGAGCTGACCA 1165
Db |||||||:|||||
1242 AAGGCGAGCCCGAGAACCAACAGGTGTACACCCCTGCCCCATCCCGGGATGAGCTGACCA 1301
QY 1166 AGAACAGGTTCAGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGG 1225
Db |||||||:|||||
1302 AGAACAGGTTCAGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCGCCGTGG 1361
QY 1226 AGTGGAGAGCAATGGGAGCCCGAGAACCAACTACAAGACACGCTCCCGTCTGGACT 1285
Db |||||||:|||||
1362 AGTGGAGAGCAATGGGAGCCCGAGAACCAACTACAAGACACGCTCCCGTCTGGACT 1421
QY 1286 CCGACGGTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGG 1345
Db |||||||:|||||
1422 CCGACGGTCTCTTCTTCTTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGG 1481
QY 1346 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGA 1405
Db |||||||:|||||
1482 GGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAAGA 1541
QY 1406 GCCTCTCCCTGTCTCGGGTAAATGA 1431
Db |||||||:|||||
1542 GCCTCTCCCTGTCTCGGGTAAATGA 1567

Search completed: June 3, 2003, 23:03:39
Job time : 194.659 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:26:38 ; Search time 81.6185 Seconds
(without alignments)
5376.898 Million cell updates/sec

Title: US-09-576-424-3
Perfect score: 1431
Sequence: 1 agaaacacctgtgttttt.....ccctgtctccgggtaataga 1431

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A COMB.seq:
2: /cgn2_6/prodata/1/ina/5B COMB.seq:
3: /cgn2_6/prodata/1/ina/6A COMB.seq:
4: /cgn2_6/prodata/1/ina/6B COMB.seq:
5: /cgn2_6/prodata/1/ina/PCUTS COMB.seq:
6: /cgn2_6/prodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1431	100.0	1431	3	US-08-487-550-3
2	1315.8	91.9	1431	3	US-08-487-550-11
3	1234.8	86.3	1567	3	US-09-049-672A-17
4	1210.4	84.6	1418	4	US-08-793-450-7
5	1171.4	81.9	1404	3	US-08-523-894-7
6	1168.2	81.6	1404	3	US-08-523-894-11
7	1166.6	81.5	1404	3	US-08-523-894-9
8	1123.6	78.5	1428	1	US-08-488-376-17
9	1123.6	78.5	1428	2	US-08-634-223-17
10	1123.6	78.5	1428	2	US-08-634-224-17
11	1123.6	78.5	1428	2	US-08-634-400-17
12	1123.6	78.5	1428	2	US-08-635-878-17
13	1123.6	78.5	1428	2	US-08-770-057-17
14	1123.6	78.5	1428	4	US-09-335-697B-17
15	1123.6	78.5	1428	4	US-09-335-697B-17
16	1117.2	78.1	1437	3	US-08-487-550-7
17	1112.4	77.7	1428	1	US-08-488-376-19
18	1112.4	77.7	1428	2	US-08-634-223-19
19	1112.4	77.7	1428	2	US-08-634-224-19
20	1112.4	77.7	1428	2	US-08-634-400-19
21	1112.4	77.7	1428	2	US-08-635-878-19
22	1112.4	77.7	1428	2	US-08-770-057-19
23	1112.4	77.7	1428	4	US-09-335-697B-19
24	1112.4	77.7	1428	4	US-09-335-697B-19
25	1111.6	77.7	19040	4	US-09-343-485A-3
26	1103.6	77.1	1617	1	US-08-378-939-9
27	1092.6	76.4	6557	1	US-08-286-740-3

28	1092.6	76.4	6557	5	PCT-US95-09576-3	Sequence 3, Appli
29	1090.6	76.2	8120	3	US-09-027-449-68	Sequence 68, Appli
30	1090.6	76.2	8120	3	US-09-026-985-68	Sequence 68, Appli
31	1090.6	76.2	8120	4	US-09-121-952A-68	Sequence 68, Appli
32	1090.6	76.2	8120	4	US-09-234-340A-68	Sequence 68, Appli
33	1090.2	76.2	1576	1	US-08-157-101A-6	Sequence 6, Appli
34	1087	76.0	9209	1	US-08-149-099C-3	Sequence 3, Appli
35	1087	76.0	9209	1	US-08-476-275-2	Sequence 3, Appli
36	1087	76.0	9209	2	US-08-478-967A-3	Sequence 3, Appli
37	1087	76.0	9209	4	US-08-475-815B-3	Sequence 3, Appli
38	1087	76.0	18986	2	US-08-819-866-2	Sequence 2, Appli
39	1087	76.0	18986	2	US-09-023-715-2	Sequence 2, Appli
40	1087	76.0	18986	4	US-09-343-485A-2	Sequence 2, Appli
41	1080.2	75.5	1350	1	US-08-157-101A-9	Sequence 9, Appli
42	1049.8	73.4	1655	3	US-09-049-672A-21	Sequence 21, Appli
43	1044.6	73.0	1135	1	US-08-236-311-8	Sequence 8, Appli
44	1044.6	73.0	1135	3	US-08-457-918-8	Sequence 8, Appli
45	1040	72.7	6285	1	US-08-467-420A-49	Sequence 49, Appli

ALIGNMENTS

RESULT 1
US-08-487-550-3
; Sequence 3, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1431 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1431
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1431
US-08-487-550-3

Query Match 100.0% ; Score 1431; DB 3; Length 1431;

i	LOCATION:	1...1431
US-08-487-550-11		
Query Match	91.9%	Score 1315.8; DB 3; Length 1431;
Best Local Similarity	95.0%	Pred. No. 3.3e-312;
Matches 1359; Conservative	0; Mismatches	72; Indels 0; Gaps 0;
Qy	1	ATGAACACCTGTGGTCTTCTCTCTCGTGGCAGCTCCAGATGGGTCTGTGTCCAG 60
Db	1	ATGAACACCTGTGGTCTTCTCTCTCGTGGCAGCTCCAGATGGGTCTGTGTCCAG 60
Qy	61	GTGAAGCTGCAGAGTGGGGCGAAGACTTTCAGCGCTTCGAGACCCCTGTCCCGCACC 120
Db	61	GTGACGCTGCAGAGTGGGGCCAGGACTGGTGAAGCCTTCGAGAGCCCTGTCCCTCACC 120
Qy	121	TGCGTTGTCTCTGTGGCTCCATCAGCGGTACTACTACTTGGACCTGGATCCGCGAGACC 180
Db	121	TGCGCTGTCTCTGTGGCTCCATCAGCGGTGTTATGGCTGGGGCTGGATCCGCGAGCCC 180
Qy	181	CCAGGAGGGGACTGGAGTGGGATATTTATGGTAAATGGTGGGACCAACAATAC 240
Db	181	CCAGGAGGGGCTGGAGTGGATGGGAGTTTCTATAGTAGTAGTGGGAACACTACTAC 240
Qy	241	AATCCCTCCCTCAAGAGTCAGAGTCAACATTTCAAAGACAGCTCCAGAACCCAGTCTTC 300
Db	241	AACCCCTCCCTCAAGAGTCAAGTCAACATTTCAAAGACAGCTCCAGAACCCAGTCTTC 300
Qy	301	CTGAACCTGAATTCGTGACCGGACCGGACACGGCCGCTCTATTACTGTGCGAGAGGCCCT 360
Db	301	CTGAAGCTGAATTCGTGACCGGCGGACACGGCCGCTCTATTACTGTGCGAGAGATCGT 360
Qy	361	CGCCCTGATTCGCAACAATTTGATGGCGGTGGTTCGATGCTGGGGCCCGGGAGAC 420
Db	361	CTTTTTTCAGTGTGGAAATGGTTTAAACAACCTGGTTCGATGCTGGGGCCCGGGAGTC 420
Qy	421	CTGGTCAACGCTCTCTCAGCTAGGACCAAGGGCCCATCGGTCTTCCCGCTGGACACCTCC 480
Db	421	CTGGTCAACGCTCTCTCAGCTAGGACCAAGGGGCCCATCGGTCTTCCCGCTGGACACCTCC 480
Qy	481	TCCAAGAGACCTCTGGGGGACAGCGGCGCTGGGCTGCTGGTTCAGAGGACTACTTCCCC 540
Db	481	TCCAAGAGACCTCTGGGGGACAGCGGCGCTGGGCTGCTGGTTCAGAGGACTACTTCCCC 540
Qy	541	GAACCGGTGACGGTGTGCGTGGAACTCAGGCGGCGCTGACAGCGGCGGTGCACCTCCCG 600
Db	541	GAACCGGTGACGGTGTGCGTGGAACTCAGGCGGCGCTGACAGCGGCGGTGCACCTCCCG 600
Qy	601	GCTGTCTTAAGTCTCTCAGGACTCTAATCTGCAAGCGGCGGTGACCGTGGCTCCAGC 660
Db	601	GCTGTCTTAAGTCTCTCAGGACTCTAATCTGCAAGCGGCGGTGACCGTGGCTCCAGC 660
Qy	661	AGCTTGGGACCCAGACCTACATCTGCAAGCGTGAATCACAAGCCCGACACCAAGGTG 720
Db	661	AGCTTGGGACCCAGACCTACATCTGCAAGCGTGAATCACAAGCCCGACACCAAGGTG 720
Qy	721	GACAAGAAAGCAGAGCCCAATCTTGTGAACAAACTCACAATGCCCGACCGTCCAGCA 780
Db	721	GACAAGAAAGCAGAGCCCAATCTTGTGAACAAACTCACAATGCCCGACCGTCCAGCA 780
Qy	781	CTTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCAAAACCCAAAGGACCCCTC 840
Db	781	CTTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCAAAACCCAAAGGACCCCTC 840
Qy	841	ATGATCTCCCGGACCCCTGAGGTACATGGTGGTGGGACGTGACCGACGAGACCTT 900
Db	841	ATGATCTCCCGGACCCCTGAGGTACATGGTGGTGGGACGTGACCGACGAGACCTT 900
Qy	901	GAGGTCAAGTTCAACTGGTACGTTGGAACGGGTGGAGGTGATATGCAAGACAAAGCCG 960
Db	901	GAGGTCAAGTTCAACTGGTACGTTGGAACGGGTGGAGGTGATATGCAAGACAAAGCCG 960
Qy	961	CGGAGGAGCAGTACAAAGACAGTACCGTGTGGTTCAGCGTCTCTCAGCTTCCTGACCCAG 1020
Db	961	CGGAGGAGCAGTACAAAGACAGTACCGTGTGGTTCAGCGTCTCTCAGCTTCCTGACCCAG 1020


```

; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1418
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..57
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 58..1418
; OTHER INFORMATION: /product= "IMMUNOGLOBIN, HEAVY"
; OTHER INFORMATION: CHAIN"
US-08-793-450-7

Query Match 84.6%; Score 1210.4; DB 4; Length 1418;
Best Local Similarity 92.4%; Pred. No. 1.8e-286;
Matches 1310; Conservative 0; Mismatches 96; Indels 12; Gaps 3;

QY 13 TGGTTCCTCTCTCTGTCGAGCTCCAGATGGTCTCTCCAGTGAAGTGCAG 72
DB 13 TGTATATCTCTCTCTTGTGTGCAACAGCTACAGGTGTCCACTCCCGAGTCCAACTGGAG 72

QY 73 CAGTGGGGGCAAGGACTTCTGAGCTTCGGAGACCTGTCCGACACCTGTCCAGTGTCTCT 132
DB 73 CAGTGGGGGCGAGGACTGTTGAAGCTTCGGAGACCTGTCCCTCACCTGCACTGTCTAT 132

QY 133 GTGTCTCCATCAGCGGTACTTACTTGGACCTGGATCCGCCAGACCCAGGGAGGGA 192
DB 133 GTGTGGTCTTCAAGTGGT---TACTTGGAGCTGGATCCGCCAGACCCAGGGAGGGG 189

QY 193 CTGGAGTGGATGGCCATATTTATGGTAAATGTTGGAGCGACCACTCAATCCCTCCCTC 252
DB 190 CTGGAGTGGATGGGGAAATCAA---TCATAGTGAAGCACCACTCAACACCCGTCCTC 246

QY 253 AAGAGTCCAGTCAACATTTCAAAGACACGTCCAAAGAACAGTCTTCTGAACTTGAAT 312
DB 247 AAGAGTCCAGTCAACATATCAGTAGACAGTCCAAAGAACAGTCTTCTGAACTGAAAC 306

QY 313 TCTGTACCGACGCGGACACCGCCCTGTATTAATGTCGAGAGGCGCCCTGCGCCCTGAATTGC 372
DB 307 TCTGTACCGCGCGGACACCGCTGTGTATTACTGTGGAGGG-----CCCCAGAGTAT 360

QY 373 ACAACCATTTGTATGGCGGCTGGGTGCATGTCTGGGGCCCGGGAGACCTGTGTACCGTTC 432
DB 361 AAATGGAAGTATCATGGGAGCTGGTTCGACCCCTGGGGCCCAAGGTACCACTGTCAACGCTC 420

QY 433 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCTCCGACACCTCTCCCAAGAGCACC 492
DB 421 TCCTCAGCTCACCAGGGCCCATCGGTCTTCCCTCCGACACCTCTCCCAAGAGCACC 480

QY 493 TCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAAGGACTACTTCCCGGAAACCGGTGACG 552
DB 481 TCTGGGGGACAGCGGCCCTGGGCTGCTGTGTCAAGGACTACTTCCCGGAAACCGGTGACG 540

QY 553 GTGTCTGTGAATCAGGGCCCTGACACGCGCGGTGCACACCTTCCCGGCTGTCTCTACAG 612
DB 541 GTGTCTGTGAATCAGGGCCCTGACACGCGCGGTGCACACCTTCCCGGCTGTCTCTACAG 600

QY 613 TCCTCAGGACTCTACTCTCCTCAGCAGCGTGGTGAACGTCCTCCAGCAGCTTGGGCACC 672
DB 601 TCCTCAGGACTCTACTCTCCTCAGCAGCGTGGTGAACGTCCTCCAGCAGCTTGGGCACC 660

```

```

QY 673 CAGACCTACATCTGCAACGTGAATCAAGGCCAGCAACCAAGGTGGAACAAGAAAGA 732
DB 661 CAGACCTACATCTGCAACGTGAATCAAGGCCAGCAACCAAGGTGGAACAAGAAAGA 720

QY 733 GAGCCCAAAATCTTGTGACAAACTCACACATGSCCCACCGTCCAGCAGCCTCAACTCCTG 792
DB 721 GAGCCCAAAATCTTGTGACAAACTCAGACATGSCCCACCGTCCAGCAGCCTCAACTCCTG 780

QY 793 GGGGACCGTCACTCTCTCTTCCCTCCCAAAACCAAGGACACCCCTCATGATCTCCCGG 852
DB 781 GGGGACCGTCACTCTCTCTTCCCTCCCAAAACCAAGGACACCCCTCATGATCTCCCGG 840

QY 853 ACCCTCAGGTACATGCTGTGTGTGAGCTGAGCAGCAGGAGACCTCTGAGTCAAGTTC 912
DB 841 ACCCTCAGGTACATGCTGTGTGTGAGCTGAGCAGCAGGAGACCTCTGAGTCAAGTTC 900

QY 913 AACTGTAGTGGACGCGGTGAGGTGCATTAATGCAAGACAAAGACCCGCGGAGGAGCAG 972
DB 901 AACTGTAGTGGACGCGGTGAGGTGCATTAATGCAAGACAAAGACCCGCGGAGGAGCAG 960

QY 973 TACAACAGCAGTACCTGCTGTGTGTGAGCTCTCTCAGCTCTGTCACAGCAGGACTGGTGAAT 1032
DB 961 TACAACAGCAGTACCTGCTGTGTGTGAGCTCTCTCAGCTCTGTCACAGCAGGACTGGTGAAT 1020

QY 1033 GGAAGAGGTACAGTGAAGTCTTCCAAAGAGCCCTCCAGCCCTCCAGCCCAATCGAGAAACC 1092
DB 1021 GGAAGAGGTACAGTGAAGTCTTCCAAAGAGCCCTCCAGCCCTCCAGCCCAATCGAGAAACC 1080

QY 1093 ATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCTCCATCCCGG 1152
DB 1081 ATCTCCAAAGCCAAAGGCGAGCCCGAGAACCAAGGTGTACACCTGCCCTCCATCCCGG 1140

QY 1153 GATGAGCTGACCAAGAACAGCTGAGCTGAGCTGAGCTGCTGCTGCTCAAGGCTTCTATCCAGC 1212
DB 1141 GATGAGCTGACCAAGAACAGCTGAGCTGAGCTGAGCTGCTGCTGCTCAAGGCTTCTATCCTAGC 1200

QY 1213 GACATGCGCTGTGAGTGGAGAGCAATGGGAGCGGAGAACAACTACAAGACCAAGCT 1272
DB 1201 GACATGCGCTGTGAGTGGAGAGCAATGGGAGCGGAGAACAACTACAAGACCAAGCT 1260

QY 1273 CCGGTGCTGAGTCCGAGCGCTCTTCTCTCTTACAGCAAGCTCAGCTGAGCAGAGC 1332
DB 1261 CCGGTGCTGAGTCCGAGCGCTCTTCTCTCTTACAGCAAGCTCAGCTGAGCAGAGC 1320

QY 1333 AGGTGGCAGAGGGAAGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCAC 1392
DB 1321 AGGTGGCAGAGGGAAGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCAC 1380

QY 1393 TACAGCAGAGAGGCTCTCTCTGCTCCGGTAAATG 1430
DB 1381 TACAGCAGAGAGGCTCTCTCTGCTCTCCGGTAAATG 1418

```

RESULT 5

```

US-08-523-894-7
; Sequence 7, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/523,894
 ; FILING DATE: 06-SEP-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-165
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1404 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT: heavy chain variable and constant gamma
 ; CHROMOSOME/SEGMENT: 4
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1404
 ; FEATURE:
 ; NAME/KEY: mat_peptide
 ; LOCATION: 1..1404
 ;

US-08-523-894-7

Query Match 81.9%; Score 1171.4; DB 3; Length 1404;
 Best Local Similarity 90.0%; Pred. No. 5.9e-277;
 Matches 1288; Conservative 0; Mismatches 116; Indels 27; Gaps 2;

QY 1 ATGAACACCTGTTCTTCTCTCTGTTGGAGCTCCAGATGGTCTCTGCCAG 60
 DB 1 ATGAACACCTGTTCTTCTCTCTGTTGGAGCTCCAGATGGTCTCTGCCAG 60
 QY 61 GTGAAGTCTCAGAGTGGGGGCAAGACTTCTGACGCTTCGGAGACCTGTCGGCACC 120
 DB 61 GTGAGCTCAGAGTGGGGGCAAGACTTCTGACGCTTCGGAGACCTGTCGGCACC 120
 QY 121 TGCAGTCTCTGTTGGTCCATCAGCGGTACTACTGACCTGGATCCGCGAGACC 180
 DB 121 TGCAGTCTCTGTTGGTCCATCAGCGGTACTACTGACCTGGATCCGCGAGACC 180
 QY 181 CCAGGAGGGGACTGAGTGGATTTGGCCATATTTATGTTATGTTGGTGGACACCAACTAC 240
 DB 181 CCAGGAGGGGACTGAGTGGATTCGCTACATCTATGTCAGTGGTGGGGGCAACCAATTAC 240
 QY 241 ATCCCTCCCTCAAGAGTCAGTCCACCATTTCAAAGACACGTCCTCAAGACCAAGTCTTC 300
 DB 241 ATCCCTCCCTCAAGAGTCAGTCCACCATTTCAAAGACACGTCCTCAAGACCAAGTCTTC 300
 QY 301 CTGAATCTGAATCTGTGACCGGACGCGGCTCTATTACTGTCGAGAGGCGCT 360
 DB 301 CTGAATCTGAATCTGTGACCGGACGCGGCTCTATTACTGTCGAGAGGCGCT 360
 QY 361 CGCCCTGATGTCACCAACATTTGTTATGGCGGCTGGGTGATGTCGTTGGGGCCCGGGAGAC 420
 DB 361 CGCCCTGATGTCACCAACATTTGTTATGGCGGCTGGGTGATGTCGTTGGGGCCCGGGAGAC 420
 QY 421 CTGTCACCGTCTCTCAGTACGACCAAGGCGCCATCGGTCTTCCCTTGGCACCCTCC 480
 DB 421 CTGTCACCGTCTCTCAGTACGACCAAGGCGCCATCGGTCTTCCCTTGGCACCCTCC 480
 QY 481 TCCAGAGACCTCTCTGGGGGACAGCGGCGCTGGGTCTGCTGCTCAAGGACTACTTCCCC 540
 DB 481 TCCAGAGACCTCTCTGGGGGACAGCGGCGCTGGGTCTGCTGCTCAAGGACTACTTCCCC 540
 QY 541 GAACCGGTGACGGTGTCTGGAACTCAGGCGCCCTGACAGCGGCGGTGACACCTTCCCG 600

DB 523 GAACCGGTGACGGTGTCTGTGAACCTCAGGGCCCTGACACGCGGTGCACACCTTCCCG 582
 QY 601 GCTGTCTTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGTGGTACCGTCCCTCCAGC 660
 DB 583 GCTGTCTTACAGTCTCTCAGGACTCTACTCTCTCAGCAGCGTGGTACCGTCCCTCCAGC 642
 QY 661 AGCTTGGGCACTCCAGACCTACATCTGCAACCTGCAATCAAGCCCGAGCAACCAAGGTG 720
 DB 643 AGCTTGGGCACTCCAGACCTACACCTGCAACCTGCAATCAAGCCCGAGCAACCAAGGTG 702
 QY 721 GACAAGAAAGCAGAGAGCCCAATCTTGTGCAAAACTCACATGCTGCCACCGTGGCCAGCA 780
 DB 703 GACAAGAGAGTGTGAGTCCAAATATATG-----TCCCCATGCCCATCATGTGCCAGCA 753
 QY 781 CCTGAACCTCTGGGGGACCGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
 DB 754 CTTGAGTCTCTGGGGGACCACTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 813
 QY 841 ATGATCTCTCCGGACCCCTGAGGTCACTGCTGGTGGTGGAGCTGAGCCAGCAAGACCT 900
 DB 814 ATGATCTCTCCGGACCCCTGAGGTCACTGCTGGTGGTGGAGCTGAGCCAGCAAGACCT 873
 QY 901 GAGTCAAGTTCAACTGTGTGAGCGGTGAGGTGAGTGCATATGCAAGCAACCAAGCGG 960
 DB 874 GAGTCCAGTTCAACTGTGTGAGCGGTGAGGTGAGTGCATATGCAAGCAACCAAGCGG 933
 QY 961 CGGAGGAGCAGTACAAACAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
 DB 934 CGGAGGAGCAGTTCAAACAGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 993
 QY 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGTCAAGTGTCTCCAAACAAAGCCCTCCAGCCCCC 1080
 DB 994 GACTGGCTGAACGCAAGGAGTACAAGTGTCAAGTGTCTCCAAACAAAGCCCTCCAGCCCCC 1053
 QY 1081 ATCAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAGAACCAAGGTGTACACCTG 1140
 DB 1054 ATCAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGAGAGAACCAAGGTGTACACCTG 1113
 QY 1141 CCCCCTCCCGGATGAGTGAACCAAGAACCAAGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
 DB 1114 CCCCCTCCCGGATGAGTGAACCAAGAACCAAGTGTGAGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
 QY 1201 TTCTATCCAGCGCATCGCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACTAC 1260
 DB 1174 TTCTATCCAGCGCATCGCGTGGAGTGGAGAGCAATGGGCGAGCCGAGAACTAC 1233
 QY 1261 AAGACAGGCTCCGCTGCTGAGTCCGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
 DB 1234 AAGACAGGCTCCGCTGCTGAGTCCGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1293
 QY 1321 GTGACAGAGCAGGTGGCAGCGGGAACGCTTCTCATGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 1380
 DB 1294 GTGACAGAGCAGGTGGCAGCGGGAACGCTTCTCATGCTCCGCTGCTGCTGCTGCTGCTGCTGCT 1353
 QY 1381 CTGCACCAACTACACGCAAGAGCT 1431
 DB 1354 CTGCACCAACTACACGCAAGAGCT 1404

RESULT 6

US-08-523-894-11
 ; Sequence 11, Application US/08523894
 ; Patent No. 6136310
 ; GENERAL INFORMATION:
 ; APPLICANT: Hanna, Nabil
 ; APPLICANT: Newman, Roland A.
 ; APPLICANT: Refi, Mitchell E.
 ; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
 ; TITLE OF INVENTION: Therapy
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

GENERAL INFORMATION:
 APPLICANT: Hanna, Nabil
 APPLICANT: Newman, Roland A.
 APPLICANT: Reff, Mitchell E.
 TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
 TITLE OF INVENTION: Therapy
 NUMBER OF SEQUENCES: 59
 CORRESPONDENCE ADDRESS:

Query Match	81.5%	Score 1166.6;	DB 3;	Length 1404;
Best Local Similarity	89.8%;	Pred. No. 8.8e-276;		
Matches 1285; Conservative	0;	Mismatches 119;	Indels 27;	Gaps 2;
1	ATGAACAACCTGTGGTTCTTCTCCTCGTGTCAGACTCCACATGSGTCTCTGCCAG	60		
/				
0	1	ATGAACAACCTGTGGTTCTTCTCCTCGTGTCAGCCCCACAGATGGGTCTTGTCGCAG	60	
/				
61	GTGAAGCTGCAGCACTGGGGCGAAGGACTTCTGCAGCCCTTCGGAGACCCTCTGCCCGACCC	120		
/				
0	61	GTGCAGCTGCAGAGAGTGGGGCCCAGGACTGTGTGAAGCCTTCGGAGACCCTGTGCCCTCACCC	120	
/				
121	TGCGTTGTCTCTGGTGGCTCCCATCAGCCGGTTACTACTCTGCACTGGATCCGCAGACCC	180		
/				
0	121	TGCAGTGTCTCTGGTGGCTCCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCAGTCC	180	
/				
181	CCAGGAGGGGACCTGGAGTGGCCATAATTTATGGTAATGTCGGACACCAAACTAC	240		
/				
0	181	CCAGGAGGGGACCTGGAGTGGATCGCTACATCTATGGCAGTGTGTGGGGGACCAAATTCAC	240	
/				
, 241	AATCCCTCCCTCAAGATCGAGTCAGCAATTTCAAAGAACAGCTCAAGAACCAGTTCTTC	300		
/				
241	AATCCCTCCCTCAACAATCGAGTCTCCAATTTCAATAGACAGCTCCAAGAACCTCTTCTCC	300		
/				

301	Qy	CTGAACTTGAAATTTCTGTGACCGACGGCGACACGGCCGCTCTATTACTGTGGAGAGGCCCT	360
301	Db		352
301	Db	CTGAAACTGAGGTCTCTGTGACCGCGCGGACACGGCCGCTCTATTACTGTGCGCA	
361	Qy	CGCCCTGATTTGCACAACTTTGTTATGCGGCTGGTGCATGTCGTGGGCGCCGGGAGAC	420
353	Db	-----GTAATATATTGAAATATCTTCACTGGTTATTATATCTTGGGCGCAGGGAGTC	402
421	Qy	CTGGTCAACCGTCTCCCTCAGCTAGCACAAAGGGCCCATCGGTCTTTCCTCCCTGGCACCCCTCC	480
403	Db		462
481	Qy	TCCAAAGACACCTCTCTGGGGGACACAGCGGCCCTGGGCTGCTGTGTCAAGGACTACTTCCCC	540
463	Db	TCCAGGAGACCTCCCGAGAGCACAGCGCCCTGGGCTGCTGTGTCAAGGACTACTTCCCC	522
541	Qy	GAACCGGTGACGCTGTCTGGGAATCAGGGGCCCTTACCAGCGGCGGTGCACACCTTCCCG	600
523	Db	GAACCGGTGACGCTGTCTGGGAATCAGGGGCCCTTACCAGCGGCGGTGCACACCTTCCCG	582
601	Qy	GCTGTCTCTCAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGTGACCGTGCCTCCAGC	660
583	Db	GCTGTCTCTCAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGTGTGACCGTGCCTCCAGC	642
661	Qy	AGCTTGGGACCCAGACCTACTCATCTCAACGTGAATCACAAGCCCAAGCAACCAACAGGTG	720
643	Db	AGCTTGGGACCAAGACCTACACCTCAACGTAGATCACAAGCCCAAGCAACCAACAGGTG	702
721	Qy	GACAAGAAAGCAGAGCCCAAACTTTGTGACAAAACTCACACATGCCCCCGTGCCAGCA	780
703	Db	GACAAGAGAGTTGAGTTCAAAATATGG-----TCCCCCATGCCCATATGCCCCAGCA	753
781	Qy	CCTGAACTCTGGGGGACCGTCAAGTCTTCTCTTCTCCCGCCCAAAACCCAAAGGACACCTC	840
754	Db	CCTGAGTTCGAGGGGGGACCATCAGTCTTCTGTCTTCTCCCGCCAAACCCAAAGGACACTCTC	813
841	Qy	ATGATCTCCCGGACCCCTGAGGTCACATCGTGGTGGTGGACGTGAGCCACGAAGACCTC	900
814	Db	ATGATCTCCCGGACCCCTGAGGTCACATCGTGGTGGTGGACGTGAGCCAGGAAGACCCC	873
901	Qy	GAGTCAAGTTCAACTGTGTTACGTGGACGGGTGGAGTGCATATGCCAAGACAAAGCCG	960
874	Db	GAGGTCCAGTTCAACTGTGTTACGTGGATGGCGTGGAGTGCATATGCCAAGACAAAGCCG	933
961	Qy	CGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTCAATCGTGGTGGACGTGAGCCACCG	1020
934	Db	CGGAGGAGCAGTTCAAACAGCAGTACCGTGTGGTCAATCGTGGTGGACGTGAGCCACCG	993
1021	Qy	GACTGGCTGAATGGCAAGGAGTACAAGTGCAGAGTCTCCAACAAAGCCCTCCAGGCCCCC	1080
994	Db	GACTGGCTGAACGGCAAGGAGTACAAGTGCAGAGTCTCCAACAAAGCCCTCCCGTCTCTCC	1053
1081	Qy	ATCGAGAAACCAATCTCCAAGCCAAAGGGCAGCCCGAGAACCAAGGTGTACACCCCTG	1140
1054	Db	ATCGAGAAACCAATCTCCAAGCCAAAGGGCAGCCCGAGAGCCACAGGTGTACACCCCTG	1113
1141	Qy	CCCCCATCCCGGATGAGCTGACCAAGAACCAAGTGCAGCTGCACCTGCTTGGTCAAGGC	1200
1114	Db	CCCCCATCCCGAGAGAGATGACCAAGAACCAAGTGCAGCTGCACCTGCTTGGTCAAGGC	1173
1201	Qy	TTCTATCCAGCACAATCGCCGTGGAGTGGGAGACAATGGGCAGCCGGAGAACAACTAC	1260
1174	Db	TTCTATCCAGCACAATCGCCGTGGAGTGGGAGACAATGGGCAGCCGGAGAACAACTAC	1233
1261	Qy	AAGACAAGCCTCCCGTGTGACTCCGACGGCTCTTCTTCTTCTTACAGAAAGTCAACC	1320
1234	Db	AAGACAAGCCTCCCGTGTGACTCCGACGGCTCTTCTTCTTCTTACAGAAAGTCAACC	1293
1321	Qy	GTGGAACAAGCAGAGTGGCAGAGGGGAAGCTTCTCATGCTCCGTGATGCATGAGGCT	1380
1294	Db	GTGGAACAAGCAGAGTGGCAGAGGGGAATGTTCTTCTCATGCTCCGTGATGCATGAGGCT	1353
1381	Qy	CTGCACAAACCACTACACGACAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA	1431

Db 1354 CTGCACACCACTACACACAGAGCCCTCTCCCTGTCTCTGGGTAAATGA 1404

RESULT 8
 US-08-488-376-17
 ; Sequence 17, Application US/08488376
 ; Patent No. 5811524
 ; GENERAL INFORMATION:
 ; APPLICANT: BRAMS, Peter
 ; APPLICANT: CHAMAT, Soulaïma Salim
 ; APPLICANT: PAN, Li-Zhen
 ; APPLICANT: WALSH, Edward E.
 ; APPLICANT: HEARD, Cheryl Janne
 ; APPLICANT: NEWMAN, Roland Anthony
 ; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
 ; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
 ; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burns, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-150
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1428 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1428
 ; US-08-488-376-17

Query Match 78.5%; Score 1123.6; DB 1; Length 1428;
 Best Local Similarity 88.5%; Pred. No. 2.8e-265;
 Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

QY 17 TCTTCTCTCTCTGTGGCAGCTCCAGATGGTCTGTCCAGGTGAAGCTGCAGCAGT 76
 DB 17 TCTTGTCTTCTCTGTGCGTGTGTACCGGTGTCTGTCCAGGTGCAGTTGCGAGGT 76

QY 77 GGGCGGAAGGACTTCTGCAGCCTTCGGAGACCTGTCCCGCACCTGCGTGTGTCTCTGGTG 136
 DB 77 CTGGTCTGTGTGTGAACCCACAGACACCTCAGCTGACCTGCACCGTCTCTGGT 136

QY 137 GCTC---CATAGCGGTACTACTGTGAACCTGANTCCGCGAGACCCAGGAGGGGAC 193
 DB 137 TCTCACTCAGCAACCTAGAAATGGGTGTGACCTGGATCCGTGATCCGTCAGCCCCCGGGAAGGCC 196

QY 194 TGGAGTGGATGGCCATATTTATGTTATGTTGGTGGCAGCACCACTACATCTCCCTCA 253
 DB 197 TAGAATGGCTTGAAACATTTTTTCGAGTGAAGAGTCTCTCTCTCTCTCTCTCTGA 253

QY 254 AGAGTCGAGTACCAATTTTCAAAGACAGCTCCAGAAACAGTTCCTTCTTGAATTT 313
 DB 254 AGAGCAGACTCACCACTCCAGGACACCTCCAGAAAGCAGGTGGTCTTAAAGCTTGACCA 313

QY 314 CTGTGACCGACGCGACACGCGCTATTACTGTGCGAGAGGCGCTCGCCCTGATTGCA 373
 DB 314 ACGTGGACCTGTGGACACAGCCACATATTACTGTGCG---ACGGGTAGGACTGTATGACA 370

QY 374 CAACCAATTTGTTATGGCGGCTGGGTGATGTCTGGGGCCCGGGAGACCTGGTCAACGCT 433
 DB 371 TCAATGCTTATTACCTATACTACCTGGATTATTGGGGCAGGAACCTTGGTCAACGCTCT 430

QY 434 CCTAGCTAGACCAAGGGCCCATCGGTCTTCCCTCTGGCACCCTCTCTCAAGAGACCT 493
 DB 431 CCTAGCTAGACCAAGGGCCCATCGGTCTTCCCTCTGGCACCCTCTCTCAAGAGACCT 490

QY 494 CTGGGGGACACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACCG 553
 DB 491 CTGGGGGACACAGCGCCCTGGGCTGCTGCTCAAGGACTACTTCCCGAACCGGTGACCG 550

QY 554 TGTCTGGAACCTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGGCTGTCTACAGT 613
 DB 551 TGTCTGGAACCTCAGCGCGCTGACAGCGGCTGCACACCTTCCCGGCTGTCTACAGT 610

QY 614 CCTCAGGACTTACTTCCCTCAGCAGCGGTGGTACCCTGCTCCAGCAGCTTTGGGACCC 673
 DB 611 CCTCAGGACTTACTTCCCTCAGCAGCGGTGGTACCCTGCTCCAGCAGCTTTGGGACCC 670

QY 674 AGACCTATCTGCAACGTGAATCAAGCCCGACCAACCAAGGTGGAGCAAGAGCAG 733
 DB 671 AGACCTATCTGCAACGTGAATCAAGCCCGACCAACCAAGGTGGAGCAAGAGCAG 730

QY 734 AGCCCAATCTTGTGACAAAACCTCACATATGCCACCGTCCAGCAGCTCTGAACTCTCTG 793
 DB 731 AGCCCAATCTTGTGACAAAACCTCACATATGCCACCGTCCAGCAGCTCTGAACTCTCTG 790

QY 794 GGGGACCGTCACTTCTTCTTCCCGGCAAAACCAAGGACACCTCATGATCTCCCGGA 853
 DB 791 GGGGACCGTCACTTCTTCTTCCCGGCAAAACCAAGGACACCTCATGATCTCCCGGA 850

QY 854 CCCCTGAGGTCACTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 913
 DB 851 CCCCTGAGGTCACTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 910

QY 914 ACTGTGACGTGGACGCGTGGAGGTGCATAATGCCAAGCAAAAGCGCGGGAGGAGCAGT 973
 DB 911 ACTGTGACGTGGACGCGTGGAGGTGCATAATGCCAAGCAAAAGCGCGGGAGGAGCAGT 970

QY 974 ACAACAGCACGTACCGTGTGGTTCAGCGTCTTCCCGTCTTCCAGCAGGACTGGTGAATG 1033
 DB 971 ACAACAGCACGTACCGTGTGGTTCAGCGTCTTCCCGTCTTCCAGCAGGAGTGGTGAATG 1030

QY 1034 GCAAGGAGTCAAGTGCAGAGTCTTCAACAAAGCCCTCCAGCCCGGCTCCAGAAACCA 1093
 DB 1031 GCAAGGAGTCAAGTGCAGAGTCTTCAACAAAGCCCTCCAGCCCGGCTCCAGAAACCA 1090

QY 1094 TCTTCAAGCCAAAGGGAGCGCCGAGAACACAGGTGTACACCTGCGCCCGGCTCCCGG 1153
 DB 1091 TCTTCAAGCCAAAGGGAGCGCCGAGAACACAGGTGTACACCTGCGCCCGGCTCCCGG 1150

QY 1154 ATGAGCTGACCAAGAACAGGTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1213
 DB 1151 ATGAGCTGACCAAGAACAGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 1210

QY 1214 ACATCGCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAGACACAGCCTC 1273
 DB 1211 ACATCGCGTGGAGTGGAGAGCAATGGGAGCGCGGAGAACAACTACAGACACAGCCTC 1270

QY 1274 CGGTCTGAGCTCCGACCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1333
 DB 1271 CGGTCTGAGCTCCGACCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1330

614 CCTCAGGACTCTACTCCCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCAACC 673
Db CCTCAGGACTCTACTCCCTCCTCAGCAGCGTGTGACCGTCCCTCCAGCAGCTTGGCAACC 670
674 AGACCTACATCTGCAAGCTGAATCAACAGCCAGCAACACCAAGGTGACCAAGAAAGCAG 733
Db AGACCTACATCTGCAAGCTGAATCAACAGCCAGCAACACCAAGGTGACCAAGAAAGCAG 730
734 AGCCCAAAATCTGTGCAAAATCTCACATGCCCCCAAAACCAAGGACCACTGATCTCCCGGA 793
Db AGCCCAAAATCTGTGCAAAATCTCACATGCCCCCAAAACCAAGGACCACTGATCTCCCGGA 790
794 GGGGACCGCTCAGTCT 853
Db GGGGACCGCTCAGTCT 850
854 CCCCTGAGGTACATGCGT 913
Db CCCCTGAGGTACATGCGT 910
914 ACTGCTAGCTGACGCGGTGAGGTGCAATGATGCAAGCAAGCAAGCGCGGAGGAGCAGT 973
Db ACTGCTAGCTGACGCGGTGAGGTGCAATGATGCAAGCAAGCAAGCGCGGAGGAGCAGT 970
974 ACAACAGCAGCTACCGT 1033
Db ACAACAGCAGCTACCGT 1030
1034 GCAAGGAGTACAGTGTGCAAGTGTGCAACAAAGCGCTCCAGCGCCCTCCAGCGCCCTCCAG 1093
Db GCAAGGAGTACAGTGTGCAAGTGTGCAACAAAGCGCTCCAGCGCCCTCCAGCGCCCTCCAG 1090
1094 TCTCCAAAGCAAGGCGAGCGCCGAGCAACACAGGTGTACACCGTCCCGCCCTCCCGGG 1153
Db TCTCCAAAGCAAGGCGAGCGCCGAGCAACACAGGTGTACACCGTCCCGCCCTCCCGGG 1150
1154 ATGAGCTGACCAAGAACAGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1213
Db ATGAGCTGACCAAGAACAGGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1210
1214 ACATCGCGTGTGAGTGTGAGAGCAATGCGGAGCGCGGAGCAACAACTACAGACCAAGCCTC 1273
Db ACATCGCGTGTGAGTGTGAGAGCAATGCGGAGCGCGGAGCAACAACTACAGACCAAGCCTC 1270
1274 CGGTGTGAGCTCCAGCGCT 1333
Db CGGTGTGAGCTCCAGCGCT 1330
1334 GTTGGCAGCAGGGAACGCT 1393
Db GTTGGCAGCAGGGAACGCT 1390
1394 ACACGAGAGAGCGCT 1431
Db ACACGAGAGAGCGCT 1428

RESULT 15

US-09-335-697B-17
; Sequence 17, Application US/09335697B
; Patent No. 6413771
; GENERAL INFORMATION:
; APPLICANT: BRAMS, Peter
; APPLICANT: CHAMAT, Souleima Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/335,697B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/770,057
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1428 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1428
US-09-335-697B-17

Query Match 78.5%; Score 1123.6; DB 4; Length 1428;

Best Local Similarity 88.5%; Pred. No. 2.8e-265;

Matches 1255; Conservative 0; Mismatches 154; Indels 9; Gaps 3;

QY 17 TCTTCT 76
Db 17 TCTTCT 76
QY 77 GGGGGAAGGACTTCTGACGCTTTCGGAGACCTGTCTCCGACCTGCGTGTGCTCTCTGTG 136
Db 77 CTGTCT 136
QY 137 GCTC---CATCAGCGGTCTACTACTGACCTGGATCCGCCAGACCCAGGAGGGGAC 193
Db 137 TCTCACTCAGCAACCTTAGAATGGGTGTGACCTGGATCCGTGAGCCCTCCCGGAGGCCC 196
QY 194 TGGAGTGAATGGCCATATTTATGTAATGTGGGACCAACCACTAATCTCTCCCTCA 253
Db 197 TAGAATGGCTTGAACAATTTTTCGAGTGCAGAGAATC---CTTCAGTCTCTCTCTGA 253
QY 254 AGAGTCAGTCAACATTTTCAAAAGACAGCTCCAGAACACAGTCTTCTCTGACTTGAATT 313
Db 254 AGAGCAGACTCACCACCTCCAGGACACCTCCAGAACACAGTCTTCTCTGACTTGAATT 313
QY 314 CTGTGACCGGACGACACGCGCTCTATTACTGTGCGAGAGGCGCTCGCCCTGATTGCA 373
Db 314 ACGTGGACCTGTGGACACAGCCACATATTACTGTGC---ACGGGTAGAGCTGTATGCA 370
QY 374 CAACCATTTGTTATGGCGGCTGGGTGCGATGCTGGGGCCCGGAGACCTGTGTACCGTCT 433
Db 371 TCAATGCTTATTACATATACCTAGTATTATGGGGCAGGGAACCTCTGTGTACCGTCT 430
QY 434 CCTCAGCTAGCACCAAGGCGCCATCGGTCTTCCCGCTGGCACCTCTCTCCAGAGCACCT 493
Db 431 CCTCAGCTAGCACCAAGGCGCCATCGGTCTTCCCGCTGGCACCTCTCTCCAGAGCACCT 490

QY 494 CTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAAACGGGTGACGG 553
Db |||||
QY 491 CTGGGGGACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAAACGGGTGACGG 550
Db |||||
QY 554 TGTGCTGGAACCTCAGCGGCCCTGACAGCGGGTGCACACCTTCCCGGCTGTCTACAGT 613
Db |||||
QY 551 TGTGCTGGAACCTCAGCGGCCCTGACAGCGGGTGCACACCTTCCCGGCTGTCTACAGT 610
Db |||||
QY 614 CCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCCCTCCAGCAGCTTGGGCACCC 673
Db |||||
QY 611 CCTCAGGACTCTACTCCCTCAGCAGCGTGTGACCCCTCCAGCAGCTTGGGCACCC 670
Db |||||
QY 674 AGACCTACATCTGCAAGCTGAATCAAGCCAGCAACCAAGGTGACAGAAAGCAG 733
Db |||||
QY 671 AGACCTACATCTGCAAGCTGAATCAAGCCAGCAACCAAGGTGACAGAAAGCAG 730
Db |||||
QY 734 AGCCCCAAATCTTGTACAAAACCTCACATGCCCCAGCGTGCACCACTGAACCTCCTGG 793
Db |||||
QY 731 AGCCCCAAATCTTGTACAAAACCTCACATGCCCCAGCGTGCACCACTGAACCTCCTGG 790
Db |||||
QY 794 GGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGA 853
Db |||||
QY 791 GGGGACCGTCACTCTTCTTCCCCCAAAACCAAGGACACCCCTCATGATCTCCCGGA 850
Db |||||
QY 854 CCCCTGAGGTACATGCGTGTGTGGAGCGTGAGCCAGAACCCCTGAGGTCAAGTTCA 913
Db |||||
QY 851 CCCCTGAGGTACATGCGTGTGTGGAGCGTGAGCCAGAACCCCTGAGGTCAAGTTCA 910
Db |||||
QY 914 ACTGCTAGCTGAGCGCGTGGAGGTGCATATGCCAAGCAAGCCGCGGAGGAGCAGT 973
Db |||||
QY 911 ACTGCTAGCTGAGCGCGTGGAGGTGCATATGCCAAGCAAGCCGCGGAGGAGCAGT 970
Db |||||
QY 974 ACAACAGCACGTACCGTGTGTGTCAGCGTCTCACCGTCTGACACAGGACTGGCTGAATG 1033
Db |||||
QY 971 ACAACAGCACGTACCGTGTGTGTCAGCGTCTCACCGTCTGACACAGGAGTGGCTGAATG 1030
Db |||||
QY 1034 GCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCA 1093
Db |||||
QY 1031 GCAAGGAGTACAAGTGCAGAGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCA 1090
Db |||||
QY 1094 TCTCCAAAGCCAAAGGGCAGCCCGAGAACACAGGTGTACACCTGCCCTCCCATCCCGG 1153
Db |||||
QY 1091 TCTCCAAAGCCAAAGGGCAGCCCGAGAACACAGGTGTACACCTGCCCTCCCATCCCGG 1150
Db |||||
QY 1154 ATGAGCTGACCAAGAACCAAGGTTCAGCTGCTGCTGCTCAAGGGCTTCTATCCAGCG 1213
Db |||||
QY 1151 ATGAGCTGACCAAGAACCAAGGTTCAGCTGCTGCTGCTCAAGGGCTTCTATCCAGCG 1210
Db |||||
QY 1214 ACATCGCGTGGAGTGGGAGAGCAATGGGACCGCGAGAACAACTACAAGACCCAGCCTC 1273
Db |||||
QY 1211 ACATCGCGTGGAGTGGGAGAGCAATGGGACCGCGAGAACAACTACAAGACCCAGCCTC 1270
Db |||||
QY 1274 CCGTGTGACTCCGACCGCTCTTCTTCTCTACAGAGCTACCGTGGACAGAGCA 1333
Db |||||
QY 1271 CCGTGTGACTCCGACCGCTCTTCTTCTCTACAGAGCTACCGTGGACAGAGCA 1330
Db |||||
QY 1334 GGTGCAGCAGGGGAAAGCTTCTCTCATGTCTCGTGCATGAGGCTCTGCACAAACCACT 1393
Db |||||
QY 1331 GGTGCAGCAGGGGAAAGCTTCTCTCATGTCTCGTGCATGAGGCTCTGCACAAACCACT 1390
Db |||||
QY 1394 ACACGAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA 1431
Db |||||
QY 1391 ACACGAGAAGAGCCTCTCCCTGTCTCCGGTAAATGA 1428
Db |||||

Search completed: June 3, 2003, 19:32:33
Job time : 87.6185 secs

THIS PAGE BLANK (USPTO)